Supplemental Material

29th November 2003

Contents

1 Primers

Table 1: Primers used in this study. Italics represent sequence complementary to the tagging cassette.

Primer Name	Source	Sequence (5' to 3')
HPM A	This study	AGGTGTTATTTCAAGGTCCTGGTGGCTTAGAAGTTTTGTTTCAGGGCCCGGCTTACCTAGTGGTGAAC
HPM B	This study	GAGCTGCGCACGTCAAGACTGTC
HPM C	This study	CCGCTCGAGGTGGCAGCCATCACCACCATCATCATCATCATCATTTGGAGGTGTTATTCAAGGTCCTG
HPM D	This study	GTGCCATATCTTCATACTATGAG
BIM1 5'	This study	GAGGTTGGCGTGAGCAACAACTTGATCATCGACGAGGAAACTTTTGGT*GGCAGCCATCACCACCATC*
BIM1 3'	This study	GGATCCAAAGAGCAATACCGAACCGCCTGAGGCACCTGCAGCAAC*GCGTTAGTATCGAATCGACAGC*
BIR1 5'	This study	GATGACAATCAATTGATCGATATTGCTAAGAAAATGGGCATTTTAGGT*GGCAGCCATCACCACCATC*
BIR1 3'	This study	TGCTATGTCAACAGTTCCCTGCAGATATCTGCGATGCGGCGAAAC*GCGTTAGTATCGAATCGACAGC*
CDC20 5'	This study	ATTCATACAAGGAGGCCCTCTAGTACCAGCCAATATTTGATCAGGGGT*GGCAGCCATCACCACCATC*
CDC20 3'	This study	CATTATGTATGCGTGTATGGAAATTTCATTATATGCCTTGACATG*GCGTTAGTATCGAATCGACAGC*
CDC5 5'	This study	ATAAAGGAAGGTTTGAAGCAGAAGTCCACAATTGTTACCGTAGATGGT*GGCAGCCATCACCACCATC*
CDC5 3'	This study	ATTAGTTATTAATGGGGCCCAATCAATGGACTGGTAATTTCGTAT*GCGTTAGTATCGAATCGACAGC*
CHK1 5'	This study	AAGAAAATTTCAACTATCTGTAGGGATATTATCCTAATTCCCAACGGT*GGCAGCCATCACCACCATC*
CHK1 3'	This study	GTTACGATGACACACTAGAAATCGAGAGAGATATATAATAAGTAG*GCGTTAGTATCGAATCGACAGC*
CLA4 5'	This study	GCATGTGATCCAAAGGATTTGACATCACTGTTGGAGTGGAAGGAAGGT*GGCAGCCATCACCACCATC*
CLA4 3'	This study	ATACATAAGATTGTAGTATGTATGATATGCTTATAGAAATAGTTG*GCGTTAGTATCGAATCGACAGC*
DBF2 5'	This study	TTATTCAACGGACTGGAACACTCAGACCCCTTTTCAACCTTTTACGGT*GGCAGCCATCACCACCATC*
DBF2 3'	This study	GCATGAAGCTCGTTAAAGCTAATTATATCGCGGCGAATGCAAGAC*GCGTTAGTATCGAATCGACAGC*
ESS1 5'	This study	ATCGTTGAATCAGGAAGCGGTGTTCATGTGATCAAGCGGGTAGGTGGT*GGCAGCCATCACCACCATC*
ESS1 3'	This study	GTTCCGCTCGCAGCGAAGAACAGCGCCATTTAACTATGTGACTAG*GCGTTAGTATCGAATCGACAGC*
GCN5 5'	This study	AATAATAAAGTAAAAGAAATACCTGAATATTCTCACCTTATTGAT*GGCAGCCATCACCACCATC*
GCN5 3'	This study	TTTCTTCTTCGAAAGGAATAGTAGCGGAAAAGCTTCTTCTACGCA*GCGTTAGTATCGAATCGAC*
GCN5–modTAP 5'	This study, [1]	AATAATAAAGTAAAAGAAATACCTGAATATTCTCACCTTATTGAT*CGGATCCCCGGGTTAATTAA*
GCN5–modTAP 3'	This study, [1]	TTTCTTCTTCGAAAGGAATAGTAGCGGAAAAGCTTCTTCTACGCA*GAATTCGAGCTCGTTTAAAC*
GLC7 5'	This study	GCCCAAAAAAGTCTACCAAGGCAAGCTGGGGGTAGAAAGAAAAAAGGT*GGCAGCCATCACCACCATC*
GLC7 3'	This study	GGAATTATTTGTGTATATGACGAGTGATGATTGCATCTTCCTTTG*GCGTTAGTATCGAATCGACAGC*
INO4 5'	This study	CCGAAGGAGTTAATTTGGGAGCTGGGTGATGGACAGAGTGGTCAG*GGCAGCCATCACCACCATC*
INO4 3'	This study	AAGAATTTCTTCGCTTATATTACTTACTTTACCCTACTCCTTGAA*GCGTTAGTATCGAATCGAC*
LTE1 5'	This study	TATATTAGCACATTAACACAAGAAGAGATTAATGAACTATCCACAGGT*GGCAGCCATCACCACCATC*
LTE1 3'	This study	ATGTATGCTCCATCTATATATGCTCCATCTGTATATTTTATATGC*GCGTTAGTATCGAATCGACAGC*

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Primer Name	Source	Sequence (5' to 3')
MAD2 5'	This study	TCTACCAACGATCATAAAGTTGGTGCGCAGGTCAGCTATAAATATGGT*GGCAGCCATCACCACCATC*
MAD2 3'	This study	AATATAGTTCATAAATCTATATTCTTTCTAAACATCGAAAACGAG*GCGTTAGTATCGAATCGACAGC*
MCD1 5'	This study	AAAATAGACGCCAAACCTGCACTATTTGAAAGGTTTATCAATGCTGGT*GGCAGCCATCACCACCATC*
MCD1 3'	This study	GTTGCCAAGATCATTCTGCCTTGCGGCCAGTAGTGGCTCTACCGC*GCGTTAGTATCGAATCGACAGC*
NBP1 5'	This study	GAAACACTTTCACCAATCTCAGTGGACTTTTCAAGTTATTTATCTGGT*GGCAGCCATCACCACCATC*
NBP1 3'	This study	GAATCATGAGGATTAGGCCGTGATCTTCGCGCTCCATATATGGAGG*CGTTAGTATCGAATCGACAGC*
PDS1 5'	This study	AGCGAAGAAGGCCTCGATCCTGAAGAACTAGAGGACTTAGTTACTGGT*GGCAGCCATCACCACCATC*
PDS1 3'	This study	AACGTACGAACAATGGCGGTAGTTGAGGTATGGGTGAGGCCGCAG*GCGTTAGTATCGAATCGACAGC*
PDS5 5'	This study	GAAGTTGACTACAAAGACGATGAAGATGATGACATCGAGATGACTGGT*GGCAGCCATCACCACCATC*
PDS5 3'	This study	CACATACATAGGCATATGTATCGCATCTTAAAGTGAGAGATCTAC*GCGTTAGTATCGAATCGACAGC*
PHO2 5'	This study	TTTTTGAAGAACACTAACGAACTAACTGACGAGCATAGATGGATA*GGCAGCCATCACCACCATC*
PHO2 3'	This study	AGGAAATACTGTTAGAGTAATATTTAGAGTTGAAAATGCAATCGC*GCGTTAGTATCGAATCGAC*
PHO4 5'	This study	GCGGCCTGCCGGTACATCCGTCACCTACAGCAGAACGTGAGCACG*GGCAGCCATCACCACCATC*
PHO4 3'	This study	GCCCCAGTCCGATATGCCCGGAACGTGCTTCCCATTGGTGCACGG*GCGTTAGTATCGAATCGAC*
RTT102 5'	This study	GTGAACAATGATAATACAAAGGAGAGTAAAGATGTGAAAATGAAT*GGCAGCCATCACCACCATC*
RTT102 3'	This study	TCCTTTACTGTAAAATAATTCTATGTGTATAAATATATAAATATA*GCGTTAGTATCGAATCGAC*
SDS22 5'	This study	TTACCTCCATCCCTACAGAAGATTGATGCGACATATATAAGAGGCGGT*GGCAGCCATCACCACCATC*
SDS22 3'	This study	GCTCGAGGTTTTTAAGGGCGAACTTTAACTAGATGGATTATTCAG*GCGTTAGTATCGAATCGACAGC*
SPO12 5'	This study	GATTCAGAGGATGTAGAAATCGATGAAGATGAGGAGTATTTCTAC*GGCAGCCATCACCACCATC*
SPO12 3'	This study	GTGTAGCATTTGGCTATTTTTGGATGACTAGAAAGGCAGATTTTT*GCGTTAGTATCGAATCGAC*
SNF2 5'	This study	TCTTTCACAGATGAAGCGGACTCGAGCATGACAGAAGCGAGTGTA*GGCAGCCATCACCACCATC*
SNF2 3'	This study	GTCTACGTATAAACGAATAAGTACTTATATTGCTTTAGGAAGGTA*GCGTTAGTATCGAATCGAC*
YAK1 5'	This study	GAAGGGCCAACAAGCGCGTTCAATAAACTTCACATTGTCGAAGAAGGT*GGCAGCCATCACCACCATC*
YAK1 3'	This study	GGCAAAATTCATATTTATTTAGTATATCATTATGGCACCAAGCCGG*CGTTAGTATCGAATCGACAGC*
YHR115C 5'	This study	ATAGACATGGAAATAAATAACAATTTAGGTGTTCGCCTAGTAGAT*GGCAGCCATCACCACCATC*
YHR115C 3'	This study	CTACAAGTTACTGTAAATGAACGAAGGAATGAACTGAAACTATTA*GCGTTAGTATCGAATCGAC*
YNL116W 5'	This study	CTTAGCGTCTTAATGGAAACTTCAAAGGATGTTGATAGCCATCCT*GGCAGCCATCACCACCATC*
YNL116W 3'	This study	TCGGTGGTTTTTCTTTATTTTTCAAACTGTGTATTTTCTTTGACC*GCGTTAGTATCGAATCGAC*
OJG84	This study, [2]	ACTTTCTGCTATTTTCACGACTTTCGATTAATTATCTGCC*CGGATCCCCGGGTTAATTAA*
OJG85	This study, [2]	CGTATAAACGAATAAGTACTTATATTGCTTTAGGAAGGTA*GAATTCGAGCTCGTTTAAAC*
OJG86	This study, [2]	CGAAGTTAAGTGTCTTGAACAACTACTATATGCATTGAAT*CGGATCCCCGGGTTAATTAA*
OJG87	This study, [2]	CACACGGATTTTGGATACACGAAGCATCTATCACGTATTC*GAATTCGAGCTCGTTTAAAC*
OJG88	This study, [2]	TTATTCTCTTAAAAGCACATTTGAAAACCATCGCCGCGAA*CGGATCCCCGGGTTAATTAA*

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Primer Name	Source	Sequence (5' to 3')
OJG89	This study, [2]	TATATATATATATATATATGCATAATACTTTTCCTTTTA*GAATTCGAGCTCGTTTAAAC*

2 Strains

Table 2: *Saccharomyces cerevisiae* strains used in this study.

Strain Name	Genotype	Source	Primers used for constr. (see table 1)
RJD 360	*MAT*a, *can1*–100, *leu2*–3,–112, *his3*–11,–15, *trp1*–1, *ura3*–1, *ade2*–1	RJD lab collection, [3]	–
RJD 415	RJD 360, *pep4*Δ::*TRP1*, *bar1*Δ::*HISG*	RJD lab collection	–
RJD 2022	RJD 415, *bim1*::BIM1–HPM::HIS3	This study	BIM1 5'/3'
RJD 2023	RJD 415, *bir1*::*BIR1*–HPM::*HIS3*	This study	BIR1 5'/3'
RJD 2024	RJD 415, *cdc20*::*CDC20*–HPM::*HIS3*	This study	CDC20 5'/3'
RJD 2026	RJD 415, *chk1*::*CHK1*–HPM::*HIS3*	This study	CHK1 5'/3'
RJD 2027	RJD 415, *cla4*::*CLA4*–HPM::*HIS3*	This study	CLA4 5'/3'
RJD 2028	RJD 415, *dbf2*::*DBF2*–HPM::*HIS3*	This study	DBF2 5'/3'
RJD 2030	RJD 415, *glc7*::*GLC7*–HPM::*HIS3*	This study	GLC7 5'/3'
RJD 2032	RJD 415, *lte1*::*LTE1*–HPM::*HIS3*	This study	LTE1 5'/3'
RJD 2033	RJD 415, *mad2*::*MAD2*–HPM::*HIS3*	This study	MAD2 5'/3'
RJD 2034	RJD 415, *mcd1*::*MCD1*–HPM::*HIS3*	This study	MCD1 5'/3'
RJD 2035	RJD 415, *nbp1*::*NBP1*–HPM::*HIS3*	This study	NBP1 5'/3'
RJD 2036	RJD 415, *pds1*::*PDS1*–HPM::*HIS3*	This study	PDS1 5'/3'
RJD 2037	RJD 415, *pds5*::*PDS5*–HPM::*HIS3*	This study	PDS5 5'/3'
RJD 2038	RJD 415, *sds22*::*SDS22*–HPM::*HIS3*	This study	SDS22 5'/3'
RJD 2039	RJD 415, *yak1*::*YAK1*–HPM::*HIS3*	This study	YAK1 5'/3'
RJD 2040	RJD 415, *yhr115c*::*YHR115C*–HPM::*HIS3*	This study	YHR115C 5'/3'
RJD 2041	RJD 415, *ynl116w*::*YNL116W*–HPM::*HIS3*	This study	YNL116W 5'/3'
RJD 2042	RJD 415, *gcn5*::*GCN5*–HPM::*HIS3*	This study	GCN5 5'/3'
RJD 2043	RJD 415, *ino4*::*INO4*–HPM::*HIS3*	This study	INO4 5'/3'
RJD 2044	RJD 415, *pho2*::*PHO2*–HPM::*HIS3*	This study	PHO2 5'/3'
RJD 2045	RJD 415, *pho4*::*PHO4*–HPM::*HIS3*	This study	PHO2 5'/3'
RJD 2046	RJD 415, *snf2*::*SNF2*–HPM::*HIS3*	This study	SNF2 5'/3'
RJD 2526	RJD 415, *spo12*::*SPO12*–HPM::*HIS3*	This study	SPO12 5'/3'
RJD 2527	RJD 415, *rtt102*::*RTT102*–HPM::*HIS3*	This study	RTT102 5'/3'
RJD 2067	S288C (*MAT*a, *his3*–1, *leu2*–0, *met15*–0, *ura3*–0), *gcn5*::*GCN5*–TAP::*His3*MX6	O'Shea lab, UCSF, [4]	–
RJD 2566	RJD 415, *snf2*Δ::*HIS3*	This study	OJG84/85
RJD 2567	RJD 415, *arp9*Δ::*HIS3*	This study	OJG86/87

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Strain Name	Genotype	Source	Primers used for constr. (see table 1)
RJD 2568	RJD 415, *rtt102*Δ::*HIS3*	This study	OJG88/89

3 Data Analysis

The listings in this document were produced by the `pdflatex` backend of `RAYzer` 3.1, using
`-s -ypd <PATH>/ypd_data_060903.tab -tab -g <PATH>/interactions.txt -moadb <PATH>/Statistika_dbase.tab -f 20.0 -b <BAIT>`.

Annotation data is extracted from the following tables:

ftp://genome-ftp.stanford.edu/pub/yeast/data_download/literature_curation/orf_geneontology.tab, timestamped 06/07/03
ftp://genome-ftp.stanford.edu/pub/yeast/data_download/protein_info/protein_properties.tab, timestamped 06/07/03
ftp://ftpmips.gsf.de/yeast/PPI/PPI_290403.tab, timestamped 04/29/03
http://biodata.mshri.on.ca:80/grid/files/download/database_data/interactions.txt, timestamped 06/06/03

Additional interaction data is **manually** retrieved from:

https://www.incyte.com/control/tools/proteome/YPDsearch-quick.html

The mass spec data presented here was filtered by `DTASelect` using these parameters:

Criterium	Value/Status
DTASelect Version	`1.9`
Data Directory	`<PATH>/<DATE>_<BAIT>`
Database searched	`<PATH>/orf_trans.fasta`, (SGD, timestamped 05/23/03)
Raw Data from	`SEQUEST v.27 in SQT format.`
DTASelect Params	`-e Contaminant --DB`
Minimum +1 XCorr	`1.8`
Minimum +2 XCorr	`2.5`
Minimum +3 XCorr	`3.5`
Minimum DeltCN	`0.08`
Minimum charge state	`1`
Maximum charge state	`3`
Minimum ion proportion	`0.0`
Maximum Sp rank	`1000`

Criterium	Value/Status
Minimum Sp score	-1.0
Modified peptide inclusion	Include
Tryptic status requirement	Any
Multiple, ambiguous IDs allowed	true
Peptide validation handling	Ignore
Purge duplicate peptides by protein	XCorr
Include only loci with unique peptide	false
Remove subset proteins	false
Locus validation handling	Ignore
Exclude protein names matching	Contaminant
Minimum modified peptides per locus	0
Minimum redundancy for low coverage loci	10
Minimum peptides per locus	2

4 Nomenclature

↑	The ORF is represented by the same set of peptides as the one preceeding it.
*	SGD associates multiple "Function" or "Process" terms with this ORF.
"NF" (not found)	SGD does not list "Length" or "CAI" information for this ORF.
"Not in SGD"	No "Function" or "Process" terms associated with the ORF in SGD. These ORFs are mostly Ty–element related.

Please note that in order to accomodate the paper format and a consumer friendly font size many of the annotation terms from `orf_geneontology.tab` had to be shortened. This resulted in occasional cryptic constructs as "sig. transd. during conjug. with cell. fus." and the shortening of e. g. "2–dehydro-3-deoxyphosphoheptonate aldolase activity" to "deoxyphosphoheptonate aldolase". When in doubt clicking on the gene/ORF name will call up the online annotation from SGD.

5 TAP–MuDPIT analysis of immune precipitations with BIM1–HPM (YER016W) as the bait protein

Table 3: Previously reported interaction partners of BIM1 (YER016W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not verified by this experiment are: TUB3/YML124C (M/G/Y, physical), MAD2/YJL030W (M/G/Y, genetic), BFA1/YJR053W (M/G/Y, genetic), MAD3/YJL013C (M/G/Y, genetic), NBP2/YDR162C (M/G/Y, genetic), PRE4/YFR050C (Y, physical), IES2/YNL215W (M/G, genetic), DAM1/YGR113W (Y, genetic), MCK1/YNL307C (M/G/Y, genetic), ARP6/YLR085C (M/G, genetic), RTT103/YDR289C (M/G, genetic), PHO23/YNL097C (M/G/Y, genetic), NUM1/YDR150W (M/G/Y, genetic), CTF3/YLR381W (M/G/Y, genetic), DCC1/YCL016C (M/G/Y, genetic), BEM1/YBR200W (M/G/Y, genetic), YGL211W (M/G, genetic), BUB3/YOR026W (M/G/Y, genetic), VAC14/YLR386W (M/G/Y, genetic), SAP30/YMR263W (M/G/Y, genetic), YGL217C (M/G/Y, genetic), SLK19/YOR195W (M/G/Y, genetic), YML094C-A (M/G/Y, genetic), VID22/YLR373C (M/G/Y, genetic), TUB1/YML085C (M/G/Y, physical), GIM5/YML094W (M/G/Y, genetic), BIK1/YCL029C (M/G/Y, gen./phys.), PAC11/YDR488C (M/G/Y, genetic), MCM22/YJR135C (M/G/Y, genetic), JNM1/YMR294W (M/G/Y, genetic), DUO1/YGL061C (M/G/Y, physical), SMI1/YGR229C (M/G/Y, genetic), DYN1/YKR054C (M/G/Y, genetic), CTF19/YPL018W (M/G/Y, genetic), BUB2/YMR055C (M/G/Y, genetic), FAB1/YFR019W (M/G/Y, genetic), ASE1/YOR058C (M/G/Y, genetic), MRC1/YCL061C (M/G/Y, genetic), MAD1/YGL086W (M/G/Y, genetic), GIM4/YEL003W (M/G/Y, genetic), PPZ1/YML016C (M/G/Y, genetic), CTF8/YHR191C (M/G/Y, genetic), YNL170W (M/G/Y, genetic), RAD54/YGL163C (M/G/Y, genetic), CHL4/YDR254W (M/G/Y, genetic), RXT2/YBR095C (M/G/Y, genetic), YDR149C (M/G, genetic), KEM1/YGL173C (M/G/Y, genetic), BUB1/YGR188C (M/G/Y, genetic), GIM3/YNL153C (M/G/Y, genetic), ARP1/YHR129C (M/G/Y, genetic), CSM3/YMR048W (M/G/Y, genetic), KIP3/YGL216W (M/G/Y, genetic), IML3/YBR107C (M/G/Y, genetic), YPL017C (M/G/Y, genetic), PAC1/YOR269W (M/G/Y, genetic), ELP2/YGR200C (M/G/Y, genetic), AOR1/YBR231C (M/G/Y, genetic), MCM21/YDR318W (M/G/Y, genetic), INP52/YNL106C (M/G/Y, genetic), YTA7/YGR270W (M/G/Y, genetic);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
BIM1/YER016W	Bait	Bait	344	0.101	82.6	88 (88)	4.55 %	struct. const. of cytoskeleton	mit. spindle checkpoint*
KAR9/YPL269W	physical	M/Y	644	0.13	14.8	7 (7)	4.55 %	mol. funct. unknown	nuclear migration

Table 4: Potential interactors recovered through TAP–MuDPIT on BIM1/YER016W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPB2/YOR151C	1224	0.228	3.1	2 (2)	4.55 %	DNA-directed RNA polymerase	transcr. from Pol II prom.

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL12B/YDR418W	165	0.766	5.5	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL12A/YEL054C	165	0.605	5.5	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL22A/YLR061W	121	0.859	32.2	2 (2)	4.55 %	struct. const. of ribosome	protein biosynthesis
RPS25A/YGR027C	108	0.716	22.2	0 (3)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS25B/YLR333C	108	0.612	22.2	↑	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS29A/YLR388W	56	0.653	33.9	1 (2)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS5/YJR123W	225	0.838	11.6	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
YGR161C-C	NF	NF	10.5	0 (2)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 5: Proteins which co–purify with BIM1/YER016W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	18.6	7 (8)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	21.6	5 (7)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	5.5	0 (2)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	10.7	2 (3)	50.00 %	alcohol dehydrogenase	fermentation
CLU1/YMR012W	1277	0.227	2.9	2 (2)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	16.8	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	17.3	4 (4)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
ILV1/YER086W	576	0.312	19.1	6 (6)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
KAR2/YJL034W	682	0.44	1.8	0 (1)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
KCS1/YDR017C	1050	0.144	7.3	6 (6)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	2.8	1 (2)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	14.7	4 (4)	95.45 %	mRNA binding	mRNA-nucleus export
RPL10/YLR075W	221	0.827	17.6	3 (3)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL13A/YDL082W	199	0.652	23.6	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL13B/YMR142C	199	0.742	23.6	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL14B/YHL001W	138	0.68	13.8	0 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	13.8	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17B/YJL177W	184	0.68	22.8	0 (3)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	184	0.809	22.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	24.3	0 (5)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	24.3	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	18.8	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	18.8	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	18.3	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL28/YGL103W	149	0.705	22.8	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL31A/YDL075W	113	0.737	34.5	0 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	34.5	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	22.3	3 (3)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	21.8	1 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	17.4	0 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL8A/YHL033C	256	0.842	12.9	0 (3)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	12.9	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	44.0	1 (9)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	44.0	1 (9)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS11B/YBR048W	156	0.733	17.3	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS11A/YDR025W	156	0.705	17.3	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS16B/YDL083C	143	0.764	23.8	0 (3)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	23.8	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS17B/YDR447C	136	0.757	20.6	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS17A/YML024W	136	0.81	20.6	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS18A/YDR450W	146	0.775	28.8	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	28.8	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	26.2	0 (4)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	26.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	12.3	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	12.3	↑	36.36 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SHM1/YBR263W	565	0.264	6.4	3 (3)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	25.5	10 (10)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	12.8	1 (6)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	13.6	0 (6)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	7.0	0 (3)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	14.0	0 (5)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	17.5	1 (6)	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	9.6	0 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	17.2	0 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	24.4	1 (6)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	24.5	0 (6)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	24.5	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	3.1	4 (4)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	4.8	0 (4)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	3.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	3.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	18.9	0 (6)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	18.9	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	18.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	3.2	0 (4)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	3.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	12.5	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	6.4	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	8.0	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	8.0	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YER160C	NF	NF	8.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	8.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	8.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	14.8	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	7.0	0 (9)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	8.7	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	8.0	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	8.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	3.3	1 (2)	54.55 %	translation elongation factor	translational elongation
YGR161C-D	NF	NF	5.9	0 (6)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.2	0 (3)	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	2.7	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	2.7	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	2.7	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	2.7	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

6 TAP–MuDPIT analysis of immune precipitations with CDC20–HPM (YGL116W) as the bait protein

Table 6: Previously reported interaction partners of CDC20 (YGL116W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: PDS1/YDR113C (Y, physical), MKK2/YPL140C (G/Y, physical), HSL1/YKL101W (M/G/Y, physical), CLB2/YPR119W (Y, physical), CIN8/YEL061C (M/G, genetic), MCD1/YDL003W (Y, genetic), MDH1/YKL085W (G/Y, physical), MAD1/YGL086W (Y, physical), CDC15/YAR019C (MIPS, genetic);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CDC20/YGL116W	Bait	Bait	610	0.140	35.1	16 (16)	9.09 %	enzyme activator	ubiquitin–dep. prot. catabol.*
CCT2/YIL142W	physical	G/Y	527	0.193	24.9	9 (9)	4.55 %	chaperone	protein folding*
CCT3/YJL014W	physical	G/Y	534	0.228	13.5	6 (6)	4.55 %	chaperone	protein folding*
CCT5/YJR064W	physical	G/Y	562	0.217	7.1	4 (4)	4.55 %	chaperone	protein folding*
MAD2/YJL030W	physical	M/G/Y	196	0.115	52.6	10 (10)	9.09 %	mol. funct. unknown	mit. spindle checkpoint
MAD3/YJL013C	physical	G/Y	515	0.128	19.2	7 (7)	4.55 %	mol. funct. unknown	mit. spindle checkpoint
TCP1/YDR212W	physical	G/Y	559	0.244	10.9	7 (7)	4.55 %	chaperone	protein folding*

Table 7: Potential interactors recovered through TAP–MuDPIT on CDC20/YGL116W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
BUB3/YOR026W	341	0.133	12.6	3 (3)	4.55 %	mol. funct. unknown	mit. spindle checkpoint
CCT4/YDL143W	528	0.225	14.2	4 (4)	9.09 %	chaperone	protein folding*
CCT6/YDR188W	546	0.177	17.0	6 (6)	4.55 %	chaperone	protein folding*
CCT7/YJL111W	550	0.192	17.8	7 (7)	4.55 %	chaperone	protein folding*
CCT8/YJL008C	568	0.203	13.4	6 (6)	9.09 %	chaperone	protein folding*
HEF3/YNL014W	1044	0.169	2.0	0 (2)	18.18 %	ATPase*	translational elongation

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ILV6/YCL009C	309	0.242	10.0	2 (2)	13.64 %	enzyme regulator*	branched chain family AA biosynth.
PNC1/YGL037C	216	0.319	13.9	2 (2)	18.18 %	nicotinamidase	chromatin silencing at telomere*
RFA1/YAR007C	621	0.206	5.3	2 (2)	4.55 %	damaged DNA binding*	DNA recombination*

Table 8: Proteins which co–purify with CDC20/YGL116W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	12.3	7 (7)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	39.9	12 (16)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	11.8	2 (6)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	9.9	2 (3)	50.00 %	alcohol dehydrogenase	fermentation
CDC19/YAL038W	500	0.893	6.0	2 (2)	50.00 %	pyruvate kinase	glycolysis*
CTS2/YDR371W	511	0.137	14.3	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	26.5	6 (6)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
ILV1/YER086W	576	0.312	6.2	2 (2)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
MIS1/YBR084W	975	0.208	4.1	3 (3)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	15.7	4 (4)	95.45 %	mRNA binding	mRNA-nucleus export
RPL31A/YDL075W	113	0.737	14.2	0 (1)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	14.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	29.3	1 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	29.3	1 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	15.1	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	15.1	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	29.2	0 (4)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	29.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	10.8	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SRO9/YCL037C	466	0.264	12.4	3 (3)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	10.9	0 (5)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	11.0	↑	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	4.4	0 (2)	72.73 %	chaperone*	response to stress*
TDH1/YJL052W	332	0.856	23.8	2 (6)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	23.8	0 (6)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	23.8	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	17.5	0 (5)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	17.5	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	5.3	3 (3)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
UGP1/YKL035W	499	0.33	8.4	3 (3)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
YAR010C	NF	NF	7.3	0 (2)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	2.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	1.8	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	1.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	7.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	6.1	3 (5)	54.55 %	translation elongation factor	translational elongation

7 TAP–MuDPIT analysis of immune precipitations with CHK1–HPM (YBR274W) as the bait protein

Known interaction partners of CHK1 (YBR274W) according to MIPS (M), GRID (G) and YPD (Y) that were not recovered in this experiment: PDS1/YDR113C (Y, physical), SAS3/YBL052C (Y, physical), SDS3/YIL084C (GRID, physical), GFD1/YMR255W (M/G/Y, physical), YNL234W (G/Y, physical), RAD9/YDR217C (G/Y, physical), YLR152C (GRID, physical), SER3/YER081W (M/G/Y, physical), CTR1/YPR124W (GRID, physical), LSM1/YJL124C (M/Y, physical), GSY2/YLR258W (M/G/Y, physical), PHO91/YNR013C (M/G/Y, physical), YPL180W (Y, physical), GFA1/YKL104C (G/Y, physical), SNX4/YJL036W (GRID, physical), RAD3/YER171W (GRID, physical);

Table 9: Potential interactors recovered through TAP–MuDPIT on CHK1/YBR274W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CHK1/YBR274W	527	0.152	50.3	21 (22)	4.55 %	protein kinase	prot. AA phosphoryl.*
ACT1/YFL039C	375	0.711	12.0	5 (5)	18.18 %	struct. const. of cytoskeleton	cell wall organ. and biogen.*
CAR2/YLR438W	424	0.292	8.0	2 (2)	13.64 %	ornithine-oxo-acid aminotransferase	arginine catabolism
GPD2/YOL059W	440	0.212	7.7	1 (2)	9.09 %	glycerol-3–P_i dehydrogenase (NAD+)	glycerol metabolism
HHT1/YBR010W	136	0.622	10.3	0 (2)	4.55 %	DNA binding	chromatin assembly/disassembly
HHT2/YNL031C	136	0.563	10.3	↑	4.55 %	DNA binding	chromatin assembly/disassembly
HTB2/YBL002W	131	0.563	11.5	0 (2)	4.55 %	DNA binding	chromatin assembly/disassembly
HTB1/YDR224C	131	0.658	11.5	↑	4.55 %	DNA binding	chromatin assembly/disassembly
HTZ1/YOL012C	134	0.17	6.7	2 (2)	4.55 %	chromatin binding	regul. of Pol II prom. transcr.*
PNC1/YGL037C	216	0.319	13.9	2 (2)	18.18 %	nicotinamidase	chromatin silencing at telomere*

Table 10: Proteins which co–purify with CHK1/YBR274W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	12.4	5 (6)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	31.0	8 (10)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	9.5	2 (4)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	10.7	3 (4)	50.00 %	alcohol dehydrogenase	fermentation
CLU1/YMR012W	1277	0.227	4.4	4 (4)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	15.3	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
HOS3/YPL116W	697	0.157	4.6	2 (2)	22.73 %	histone deacetylase	histone deacetylation
KAR2/YJL034W	682	0.44	4.8	0 (2)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
MIS1/YBR084W	975	0.208	6.1	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	19.1	6 (6)	95.45 %	mRNA binding	mRNA-nucleus export
PSA1/YDL055C	361	0.6	14.4	3 (3)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL28/YGL103W	149	0.705	20.1	3 (3)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL31A/YDL075W	113	0.737	24.8	0 (3)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	24.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	9.4	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	9.4	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	29.3	1 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	29.3	1 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS15/YOL040C	142	0.769	21.1	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	30.8	0 (5)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	30.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS4B/YHR203C	261	0.709	11.5	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.5	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SRO9/YCL037C	466	0.264	14.4	4 (4)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	6.5	0 (3)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	8.9	1 (4)	100.00 %	heat shock protein	protein folding*
SSA4/YER103W	642	0.184	4.4	0 (2)	72.73 %	chaperone*	response to stress*
TDH1/YJL052W	332	0.856	13.9	0 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	21.4	0 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	25.9	1 (6)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	8.3	0 (4)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	8.3	↑	90.91 %	translation elongation factor	translational elongation

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
TFP1/YDL185W	1071	0.305	3.2	2 (2)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
URA2/YJL130C	2214	0.286	2.3	3 (3)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR010C	NF	NF	10.2	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	10.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	10.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	3.3	0 (4)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	3.3	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	3.3	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	3.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	3.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	3.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	3.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	3.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	3.3	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	3.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

8 TAP–MuDPIT analysis of immune precipitations with CLA4–HPM (YNL298W) as the bait protein

Table 11: Previously reported interaction partners of CLA4 (YNL298W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: ARC40/YBR234C (M/G, genetic), UBA4/YHR111W (Y, genetic), SLK19/YOR195W (Y, genetic), FKH2/YNL068C (Y, genetic), URE2/YNL229C (Y, genetic), RIM20/YOR275C (Y, genetic), RPS21B/YJL136C (Y, genetic), ELP6/YMR312W (Y, genetic), RPL35A/YDL191W (Y, genetic), PRE9/YGR135W (Y, genetic), ELP2/YGR200C (Y, genetic), GIC1/YHR061C (M/G/Y, physical), CDC24/YAL041W (Y, physical), ARP2/YDL029W (M/G, genetic), SWI4/YER111C (Y, genetic), ABP1/YCR088W (M/G/Y, physical), SWD3/YBR175W (Y, genetic), ASF1/YJL115W (Y, genetic), DCC1/YCL016C (Y, genetic), PCL2/YDL127W (Y, genetic), BEM1/YBR200W (Y, gen./phys.), SLA2/YNL243W (M/Y, physical), RPL24A/YGL031C (Y, genetic), CDC28/YBR160W (Y, physical), DYN2/YDR424C (Y, genetic), CTF8/YHR191C (Y, genetic), PHO85/YPL031C (Y, genetic), ZDS2/YML109W (M/Y, physical), YML094C-A (Y, genetic), BEM3/YPL115C (M/G/Y, physical), ITC1/YGL133W (Y, genetic), MGA2/YIR033W (Y, genetic), GIM5/YML094W (Y, genetic), STE20/YHL007C (M/Y, genetic), BEM4/YPL161C (Y, genetic), SPO12/YHR152W (Y, genetic), CHS7/YHR142W (Y, genetic), CTF4/YPR135W (Y, genetic), BNI1/YNL271C (M/G/Y, genetic), CDC42/YLR229C (M/G/Y, gen./phys.), RRD1/YIL153W (Y, genetic), HOS4/YIL112W (Y, genetic), SLT2/YHR030C (Y, genetic), CLN1/YMR199W (M/Y, genetic), YGL211W (Y, genetic), GIC2/YDR309C (M/G/Y, physical), PEA2/YER149C (Y, genetic), CHS5/YLR330W (Y, genetic), BOI2/YER114C (M/G/Y, physical), YBL062W (Y, genetic), YPL047W (Y, genetic), UBP8/YMR223W (Y, genetic), YBR174C (Y, genetic), CDC12/YHR107C (M/G/Y, gen./phys.), RXT2/YBR095C (Y, genetic), FAB1/YFR019W (Y, genetic), CHS6/YJL099W (Y, genetic), SMI1/YGR229C (Y, genetic), RAD54/YGL163C (Y, genetic), IXR1/YKL032C (Y, genetic), RGA1/YOR127W (M/Y, physical), RTT106/YNL206C (Y, genetic), SEM1/YDR363W-A (Y, genetic), RTT101/YJL047C (Y, genetic), SIT4/YDL047W (Y, genetic), PCL1/YNL289W (Y, genetic), NUP100/YKL068W (GRID, physical), SGF73/YGL066W (Y, genetic), EDE1/YBL047C (Y, genetic), GIM3/YNL153C (Y, genetic), BEM2/YER155C (Y, genetic), AKR1/YDR264C (Y, genetic), CLN2/YPL256C (M/Y, genetic), BCK1/YJL095W (Y, genetic), VAC14/YLR386W (Y, genetic), SHS1/YDL225W (Y, genetic), MSB2/YGR014W (M/Y, physical), NIP100/YPL174C (Y, genetic), APC9/YLR102C (Y, genetic), SAP30/YMR263W (Y, genetic), SPA2/YLL021W (Y, genetic), BUD6/YLR319C (Y, genetic), CHS3/YBR023C (Y, genetic), SKT5/YBL061C (Y, genetic), RPN10/YHR200W (Y, genetic);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CLA4/YNL298W	Bait	Bait	842	0.131	53.6	42 (44)	4.55 %	prot. Ser/Thr kin.	prot. AA phosphoryl.*
RPL17B/YJL177W	genetic	Y	184	0.68	15.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	genetic	Y	184	0.809	15.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	genetic	Y	189	0.708	13.2	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	genetic	Y	189	0.686	13.2	↑	50.00 %	struct. const. of ribosome	protein biosynthesis

Table 12: Potential interactors recovered through TAP–MuDPIT on CLA4/YNL298W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PBP1/YGR178C	722	0.168	4.6	2 (2)	9.09 %	mol. funct. unknown	mRNA polyadenylation
PRE8/YML092C	250	0.143	12.8	2 (2)	4.55 %	endopeptidase	ubiquitin–dep. prot. catabol.
RPL36A/YMR194W	100	0.62	24.0	0 (2)	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL36B/YPL249C-A	100	0.8	24.0	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL7A/YGL076C	244	0.76	18.0	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL7B/YPL198W	244	0.716	18.0	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPP2A/YOL039W	106	0.804	21.7	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RPS2/YGL123W	254	0.801	7.1	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis*
SEC23/YPR181C	768	0.229	3.9	2 (2)	18.18 %	GTPase activator	ER to Golgi transport*
SKM1/YOL113W	655	0.112	4.7	1 (2)	4.55 %	prot. Ser/Thr kin.	prot. AA phosphoryl.*
YBR225W	900	0.141	2.4	2 (2)	9.09 %	mol. funct. unknown	biological process unknown
YHB1/YGR234W	399	0.267	8.0	2 (2)	18.18 %	mol. funct. unknown	response to stress

Table 13: Proteins which co–purify with CLA4/YNL298W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	22.4	7 (9)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	5.5	0 (2)	72.73 %	alcohol dehydrogenase	fermentation*
CDC19/YAL038W	500	0.893	8.6	2 (2)	50.00 %	pyruvate kinase	glycolysis*
CTS2/YDR371W	511	0.137	17.2	6 (6)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	19.2	4 (4)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HSC82/YMR186W	705	0.581	4.0	0 (2)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	3.9	↑	27.27 %	chaperonin ATPase	response to stress*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
IMD1/YAR073W	403	0.287	8.4	0 (2)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD2/YHR216W	523	0.305	6.5	0 (2)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD3/YLR432W	523	0.464	6.5	↑	27.27 %	IMP dehydrogenase	GTP biosynthesis
MIS1/YBR084W	975	0.208	8.9	7 (8)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	20.0	6 (6)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	6.5	4 (4)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	3.1	2 (2)	31.82 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	4.9	2 (2)	31.82 %	serine-type endopeptidase	sporulation*
PSA1/YDL055C	361	0.6	13.3	3 (3)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL10/YLR075W	221	0.827	13.6	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL13A/YDL082W	199	0.652	20.6	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	20.6	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL14B/YHL001W	138	0.68	21.7	0 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	21.7	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL15A/YLR029C	204	0.783	20.6	0 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	20.6	↑	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL16B/YNL069C	198	0.723	13.6	2 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL18B/YNL301C	186	0.68	14.5	0 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	14.5	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL1B/YGL135W	217	0.832	12.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	12.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	23.3	0 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	24.1	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	10.6	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	10.6	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	18.3	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	18.4	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	18.4	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	39.6	6 (6)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	28.0	0 (6)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	28.0	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	15.5	4 (4)	40.91 %	struct. const. of ribosome	protein biosynthesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL31A/YDL075W	113	0.737	23.9	0 (3)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	23.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	23.8	4 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	18.5	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	18.5	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6A/YML073C	176	0.672	20.5	1 (3)	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL6B/YLR448W	176	0.627	14.2	0 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	8.6	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	8.6	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	24.1	0 (5)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	24.1	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	9.0	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS13/YDR064W	151	0.776	23.8	3 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS14A/YCR031C	137	0.805	32.1	0 (3)	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS14B/YJL191W	138	0.59	31.9	↑	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS15/YOL040C	142	0.769	30.3	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS17B/YDR447C	136	0.757	40.4	0 (4)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS17A/YML024W	136	0.81	40.4	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS18A/YDR450W	146	0.775	21.2	0 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	21.2	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	12.2	1 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	11.8	1 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	19.0	2 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	36.9	0 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	36.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS24A/YER074W	135	0.816	17.8	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS24B/YIL069C	135	0.756	17.8	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26B/YER131W	119	0.711	20.2	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26A/YGL189C	119	0.781	20.2	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	31.2	4 (4)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS31/YLR167W	152	0.811	17.8	1 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPS4B/YHR203C	261	0.709	29.1	0 (5)	59.09 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS4A/YJR145C	261	0.695	29.1	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	20.8	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	20.8	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	22.8	9 (9)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	13.9	4 (4)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	8.7	0 (4)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	10.8	1 (5)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	6.8	1 (3)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	4.4	0 (2)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	15.0	1 (6)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	15.0	↑	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	9.6	0 (2)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	25.6	0 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	31.3	1 (6)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	9.0	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	9.0	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	3.4	5 (5)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	6.0	0 (5)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	4.1	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	4.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	18.0	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	4.6	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	13.2	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	13.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	13.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	13.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	13.2	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	6.5	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YER160C	NF	NF	6.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	8.1	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	7.4	0 (9)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	7.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	8.4	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	9.3	0 (11)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	3.3	3 (3)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	9.3	0 (11)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	7.7	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	10.5	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	7.4	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	3.2	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.8	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	6.0	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	6.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	6.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	4.4	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	6.0	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

9 TAP–MuDPIT analysis of immune precipitations with DBF2–HPM (YGR092W) as the bait protein

Table 14: Previously reported interaction partners of DBF2 (YGR092W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: TEM1/YML064C (Y, genetic), SIC1/YLR079W (M/G/Y, genetic), YLR424W (M/G/Y, physical), CDC5/YMR001C (Y, genetic), CDC36/YDL165W (Y, physical), CYR1/YJL005W (G/Y, physical), CDC12/YHR107C (Y, physical), POP2/YNR052C (M/G/Y, physical), RPN5/YDL147W (G/Y, physical), DHH1/YDL160C (M/G, physical), GPH1/YPR160W (G/Y, physical), SWI5/YDR146C (M/G/Y, genetic), SSN3/YPL042C (Y, physical), CAF17/YJR122W (Y, physical), YJR072C (G/Y, physical), YKL061W (M/G/Y, physical), CDC15/YAR019C (M/G, genetic), SIT4/YDL047W (M/G, genetic), CCR4/YAL021C (M/G/Y, physical), NOT5/YPR072W (Y, physical), RPT5/YOR117W (G/Y, physical), FAA1/YOR317W (G/Y, physical), CDC39/YCR093W (Y, physical), SEC27/YGL137W (G/Y, physical), MOT2/YER068W (Y, physical), TPS1/YBR126C (G/Y, physical), RPT3/YDR394W (G/Y, physical), SPO12/YHR152W (M/G/Y, genetic), CAF40/YNL288W (Y, physical), CAF4/YKR036C (Y, physical), NOT3/YIL038C (Y, physical), SSN8/YNL025C (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
DBF2/YGR092W	Bait	Bait	572	0.141	43.9	29 (37)	4.55 %	protein kinase	prot. AA phosphoryl.*
DBF20/YPR111W	genetic	M/G/Y	564	0.138	8.9	0 (8)	4.55 %	prot. Ser/Thr kin.	prot. AA phosphoryl.*
MOB1/YIL106W	gen./phys.	M/G/Y	314	0.105	51.6	22 (22)	4.55 %	kinase regulator	prot. AA phosphoryl.*
TFP1/YDL185W	physical	G/Y	1071	0.305	9.7	6 (6)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*

Table 15: Potential interactors recovered through TAP–MuDPIT on DBF2/YGR092W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH5/YBR145W	351	0.253	2.3	0 (2)	4.55 %	alcohol dehydrogenase	alcohol metabolism
CAF20/YOR276W	161	0.356	17.4	2 (2)	18.18 %	translation regulator	negative regulation of translation
CAR2/YLR438W	424	0.292	8.0	2 (2)	13.64 %	ornithine-oxo-acid aminotransferase	arginine catabolism
CDC33/YOL139C	213	0.387	10.3	2 (2)	13.64 %	translation initiation factor	translational initiation*
EMI2/YDR516C	500	0.178	6.6	2 (2)	9.09 %	mol. funct. unknown	biological process unknown

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
GFA1/YKL104C	717	0.272	5.9	2 (2)	9.09 %	glucosamine–fructose–6–P_i aminotransf.	cell wall chitin biosynthesis
GLY1/YEL046C	387	0.33	11.9	3 (3)	18.18 %	threonine aldolase	threonine catabolism*
GPD2/YOL059W	440	0.212	11.8	2 (3)	9.09 %	glycerol-3–P_i dehydrogenase (NAD+)	glycerol metabolism
HSP42/YDR171W	375	0.182	9.1	2 (2)	9.09 %	chaperone*	response to stress*
ILV6/YCL009C	309	0.242	16.8	3 (3)	13.64 %	enzyme regulator*	branched chain family AA biosynth.
PNC1/YGL037C	216	0.319	13.9	2 (2)	18.18 %	nicotinamidase	chromatin silencing at telomere*
PRO1/YDR300C	428	0.198	9.1	2 (2)	9.09 %	glutamate 5-kinase	proline biosynthesis
RIB4/YOL143C	169	0.211	32.5	3 (3)	13.64 %	6,7-dimethyl-8-ribityllumazine synthase	vitamin B2 biosynthesis
SEC23/YPR181C	768	0.229	6.5	3 (3)	18.18 %	GTPase activator	ER to Golgi transport*
SHM2/YLR058C	469	0.589	15.1	6 (6)	13.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SNF1/YDR477W	633	0.188	5.4	2 (2)	18.18 %	SNF1A/AMP-activ. prot. kinase	prot. AA phosphoryl.*
TRP3/YKL211C	484	0.184	4.8	2 (2)	13.64 %	anthranilate synthase*	tryptophan biosynthesis
TUB2/YFL037W	457	0.271	5.5	2 (2)	13.64 %	struct. const. of cytoskeleton	mitotic chromosome segregation*

Table 16: Proteins which co–purify with DBF2/YGR092W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	18.0	8 (8)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	41.7	13 (16)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	9.8	2 (5)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	8.8	2 (2)	50.00 %	alcohol dehydrogenase	fermentation
ASN2/YGR124W	572	0.317	6.1	2 (3)	22.73 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
CTS2/YDR371W	511	0.137	10.2	3 (3)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	27.0	6 (6)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HSC82/YMR186W	705	0.581	6.8	0 (3)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	6.8	↑	27.27 %	chaperonin ATPase	response to stress*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ILV1/YER086W	576	0.312	12.8	4 (4)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
MIS1/YBR084W	975	0.208	6.9	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	19.1	5 (5)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	5.6	3 (3)	63.64 %	6-phosphofructokinase	glycolysis
PSA1/YDL055C	361	0.6	30.7	6 (6)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL28/YGL103W	149	0.705	17.4	2 (2)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL31A/YDL075W	113	0.737	33.6	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	33.6	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	14.1	0 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	24.1	1 (3)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS15/YOL040C	142	0.769	21.1	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	19.2	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	19.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
SRO9/YCL037C	466	0.264	26.4	8 (8)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	26.2	1 (10)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	35.7	4 (14)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	7.9	0 (3)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	10.7	0 (4)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	5.1	0 (2)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	5.1	↑	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	17.2	1 (5)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	34.6	1 (10)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	54.8	8 (17)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	21.0	0 (9)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	21.0	↑	90.91 %	translation elongation factor	translational elongation
TRP5/YGL026C	707	0.32	7.6	3 (3)	22.73 %	tryptophan synthase	tryptophan biosynthesis
UGP1/YKL035W	499	0.33	18.2	7 (7)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	1.8	2 (2)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
VMA2/YBR127C	517	0.39	17.0	5 (5)	22.73 %	H^+–exporting ATPase	vacuolar acidification
YBL005W-B	NF	NF	1.4	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YER138C	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	1.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	1.4	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	1.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

10 TAP–MuDPIT analysis of immune precipitations with GCN5–HPM (YGR252W) as the bait protein

Table 17: Previously reported interaction partners of GCN5 (YGR252W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: SRB4/YER022W (Y, physical), YAP1/YML007W (Y, physical), FBA1/YKL060C (Y, physical), MYO1/YHR023W (Y, physical), PFK2/YMR205C (Y, physical), TAF13/YML098W (Y, physical), CYC8/YBR112C (Y, physical), TAF2/YCR042C (Y, physical), SNF2/YOR290C (M/G, genetic), SPT15/YER148W (Y, physical), SRB8/YCR081W (Y, physical), RGR1/YLR071C (Y, physical), HHT1/YBR010W (Y, gen./phys.), PUF6/YDR496C (Y, physical), MED11/YMR112C (Y, physical), MOT1/YPL082C (Y, physical), AFR1/YDR085C (Y, genetic), SWI1/YPL016W (M/G/Y, genetic), SIN4/YNL236W (M/G/Y, gen./phys.), VPS1/YKR001C (Y, physical), ENO2/YHR174W (Y, physical), YIL077C (Y, physical), RVB2/YPL235W (Y, physical), PSK1/YAL017W (Y, physical), MLP1/YKR095W (Y, physical), MED2/YDL005C (Y, physical), YOR225W (M/G/Y, physical), MED4/YOR174W (Y, physical), TAF7/YMR227C (Y, physical), HEM13/YDR044W (Y, physical), SRB2/YHR041C (M/G/Y, gen./phys.), VAS1/YGR094W (Y, physical), RTG2/YGL252C (Y, physical), KAP123/YER110C (Y, physical), NUT1/YGL151W (Y, physical), HAC1/YFL031W (Y, physical), MRPL6/YHR147C (Y, physical), TAF1/YGR274C (Y, physical), SIN3/YOL004W (Y, physical), HHT2/YNL031C (Y, physical), TAF3/YPL011C (Y, physical), SSN2/YDR443C (Y, physical), ADR1/YDR216W (MIPS, physical), KAP114/YGL241W (Y, physical), SSN8/YNL025C (Y, physical), FUN19/YAL034C (Y, physical), ROX3/YBL093C (Y, physical), IRE1/YHR079C (M/Y, physical), TAF11/YML015C (Y, physical), NOP1/YDL014W (Y, physical), SSN3/YPL042C (Y, physical), PGK1/YCR012W (Y, physical), SRB6/YBR253W (G/Y, physical), PTC1/YDL006W (Y, physical), CTI6/YPL181W (Y, physical), RPT5/YOR117W (Y, physical), COG3/YER157W (Y, physical), MED6/YHR058C (Y, physical), TAF4/YMR005W (Y, physical), RPB9/YGL070C (Y, genetic), TIF1/YKR059W (Y, physical), FAB1/YFR019W (Y, physical), HHF2/YNL030W (Y, physical), TAF14/YPL129W (Y, physical), MED1/YPR070W (Y, physical), YNG2/YHR090C (Y, genetic), SNF5/YBR289W (M/G, genetic), RPB2/YOR151C (Y, physical), MED8/YBR193C (Y, physical), FET4/YMR319C (G/Y, physical), SRB5/YGR104C (Y, physical), GAL11/YOL051W (Y, physical), SRP1/YNL189W (Y, physical), MYO4/YAL029C (Y, physical), RPG1/YBR079C (Y, physical), SAS3/YBL052C (Y, genetic), CLU1/YMR012W (Y, physical), CSE2/YNR010W (Y, physical), PGD1/YGL025C (Y, physical), SRB7/YDR308C (Y, physical), SSE2/YBR169C (Y, physical), TAF8/YML114C (Y, physical), RPO21/YDL140C (Y, physical), TBF1/YPL128C (Y, physical), MNN4/YKL201C (Y, physical), RPN9/YDR427W (Y, physical), NUT2/YPR168W (Y, physical), TEF4/YKL081W (Y, physical), HHF1/YBR009C (Y, genetic), MED7/YOL135C (Y, physical), MES1/YGR264C (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
GCN5/YGR252W	Bait	Bait	439	0.121	68.6	65 (65)	4.55 %	histone acetyltransferase	histone acetylation*
ADA2/YDR448W	physical	M/G/Y	434	0.119	57.1	36 (36)	4.55 %	transcr. co-activator	histone acetylation*
ADH1/YOL086C	physical	Y	348	0.811	10.9	2 (4)	86.36 %	alcohol dehydrogenase	fermentation
AHC1/YOR023C	physical	Y	566	0.145	46.1	22 (22)	4.55 %	mol. funct. unknown	nucleosome disassembly
HFI1/YPL254W	physical	M/G/Y	488	0.115	53.9	23 (23)	4.55 %	transcr. cofactor	transcr. from Pol II prom.*
NGG1/YDR176W	gen./phys.	M/G/Y	702	0.133	66.4	53 (53)	4.55 %	transcr. cofactor	histone acetylation*
SGF29/YCL010C	physical	G/Y	259	0.104	51.4	17 (17)	4.55 %	mol. funct. unknown	histone acetylation
SGF73/YGL066W	physical	Y	657	0.132	35.8	18 (18)	4.55 %	mol. funct. unknown	histone acetylation
SPT20/YOL148C	physical	M/G/Y	604	0.111	53.3	26 (26)	4.55 %	transcr. cofactor	histone acetylation*

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Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SPT3/YDR392W	physical	M/Y	337	0.135	27.0	12 (12)	4.55 %	transcr. cofactor	pseudohyphal growth*
SPT7/YBR081C	physical	M/G/Y	1332	0.154	26.5	28 (28)	4.55 %	struct. molecule	conjug. with cell. fusion*
SPT8/YLR055C	physical	M/Y	602	0.124	51.5	23 (23)	4.55 %	transcr. cofactor	histone acetylation*
TAF10/YDR167W	physical	M/G/Y	206	0.096	46.6	9 (9)	4.55 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
TAF12/YDR145W	physical	M/Y	539	0.115	32.5	16 (16)	4.55 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
TAF5/YBR198C	physical	M/Y	798	0.129	51.4	35 (35)	4.55 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
TAF6/YGL112C	physical	M/G/Y	516	0.147	47.9	23 (23)	4.55 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
TAF9/YMR236W	physical	M/Y	157	0.082	68.8	7 (7)	4.55 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
TRA1/YHR099W	physical	M/G/Y	3744	0.139	13.8	35 (35)	4.55 %	histone acetyltransferase	regul. of Pol II prom. transcr.*
UBP8/YMR223W	physical	G/Y	471	0.163	30.8	13 (13)	4.55 %	ubiquitin–spec. protease	protein deubiquitination

Table 18: Potential interactors recovered through TAP–MuDPIT on GCN5/YGR252W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADE3/YGR204W	946	0.277	2.1	0 (2)	9.09 %	formate-tetrahydrofolate ligase	purine base biosynthesis
EFT2/YDR385W	842	0.8	4.0	0 (2)	18.18 %	translation elongation factor	translational elongation
EFT1/YOR133W	842	0.804	4.0	↑	18.18 %	translation elongation factor	translational elongation
GFA1/YKL104C	717	0.272	5.6	2 (2)	9.09 %	glucosamine–fructose–6–P_i aminotransf.	cell wall chitin biosynthesis
GLC7/YER133W	312	0.229	30.4	7 (7)	13.64 %	protein phosphatase type 1*	meiosis*
MSN4/YKL062W	630	0.16	10.0	5 (5)	4.55 %	transcr. factor*	response to stress*
PPZ2/YDR436W	710	0.109	6.9	2 (2)	13.64 %	protein Ser/Thr phosphatase	sodium ion homeostasis
RPL16A/YIL133C	199	0.611	13.6	2 (2)	13.64 %	struct. const. of ribosome*	protein biosynthesis
RPP2A/YOL039W	106	0.804	31.1	3 (3)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RPP2B/YDR382W	110	0.762	20.0	2 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS25A/YGR027C	108	0.716	19.4	0 (2)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS25B/YLR333C	108	0.612	19.4	↑	13.64 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS29B/YDL061C	56	0.76	33.9	1 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
SDS22/YKL193C	338	0.182	49.7	9 (9)	13.64 %	enzyme regulator*	chromosome segregation*
SOD2/YHR008C	233	0.226	12.0	2 (2)	4.55 %	manganese superoxide dismutase	oxygen and ROS metabolism
TFC1/YBR123C	649	0.135	8.0	2 (2)	4.55 %	RNA polymerase III transcr. factor	transcr. initiation from Pol III prom.
TRP3/YKL211C	484	0.184	9.5	3 (3)	13.64 %	anthranilate synthase*	tryptophan biosynthesis
TUB2/YFL037W	457	0.271	9.6	3 (3)	13.64 %	struct. const. of cytoskeleton	mitotic chromosome segregation*
URA7/YBL039C	579	0.309	23.8	9 (10)	13.64 %	CTP synthase	phospholipid biosynthesis*
YCR082W	128	0.159	67.2	16 (16)	4.55 %	mol. funct. unknown	biological process unknown
YHB1/YGR234W	399	0.267	7.8	2 (2)	18.18 %	mol. funct. unknown	response to stress
YPI1/YFR003C	155	0.121	17.4	2 (2)	13.64 %	mol. funct. unknown	biological process unknown
YPL047W	99	0.122	32.3	3 (3)	4.55 %	mol. funct. unknown	biological process unknown
YPL137C	1276	0.164	4.0	2 (2)	9.09 %	mol. funct. unknown	biological process unknown
YSH1/YLR277C	779	0.147	4.9	2 (2)	4.55 %	cleav./polyadenyl. specif. fact.	mRNA polyadenylation*

Table 19: Proteins which co–purify with GCN5/YGR252W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH2/YMR303C	348	0.505	5.5	0 (2)	72.73 %	alcohol dehydrogenase	fermentation*
CDC19/YAL038W	500	0.893	6.0	2 (2)	50.00 %	pyruvate kinase	glycolysis*
CTS2/YDR371W	511	0.137	31.9	11 (11)	81.82 %	mol. funct. unknown	biological process unknown
ILV1/YER086W	576	0.312	10.2	3 (3)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
IMD1/YAR073W	403	0.287	12.4	1 (2)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD3/YLR432W	523	0.464	8.4	1 (2)	27.27 %	IMP dehydrogenase	GTP biosynthesis
KCS1/YDR017C	1050	0.144	15.6	10 (10)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	25.0	14 (16)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	21.3	8 (8)	95.45 %	mRNA binding	mRNA-nucleus export

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PFK1/YGR240C	987	0.466	7.7	4 (4)	63.64 %	6-phosphofructokinase	glycolysis
PSA1/YDL055C	361	0.6	12.5	4 (4)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL10/YLR075W	221	0.827	33.5	6 (6)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL13A/YDL082W	199	0.652	10.1	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	24.6	1 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL14B/YHL001W	138	0.68	22.5	0 (3)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	22.5	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL15A/YLR029C	204	0.783	18.6	1 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	13.7	0 (2)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL16B/YNL069C	198	0.723	13.6	2 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17A/YKL180W	184	0.809	21.2	1 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL17B/YJL177W	184	0.68	15.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL18B/YNL301C	186	0.68	14.5	0 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	14.5	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	13.8	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	13.8	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL1B/YGL135W	217	0.832	12.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	12.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	42.2	0 (8)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	43.7	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	23.8	1 (5)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	21.9	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	9.2	1 (1)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL28/YGL103W	149	0.705	39.6	6 (6)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	41.3	0 (10)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	41.3	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	17.6	5 (5)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	47.8	1 (8)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	47.8	1 (8)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	23.8	4 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL40A/YIL148W	128	0.742	36.7	0 (4)	18.18 %	struct. const. of ribosome*	protein biosynthesis*
RPS31/YLR167W	152	0.811	30.9	↑	31.82 %	struct. const. of ribosome*	protein biosynthesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
UBI4/YLL039C	381	0.317	12.3	↑	22.73 %	protein tagging*	response to stress*
RPL40B/YKR094C	128	0.742	36.7	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis*
RPL4A/YBR031W	362	0.803	34.8	0 (6)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	34.8	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6B/YLR448W	176	0.627	18.8	0 (3)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL6A/YML073C	176	0.672	18.8	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	33.2	2 (6)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	27.7	0 (4)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	43.5	2 (10)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	39.8	1 (9)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	15.7	4 (4)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS11B/YBR048W	156	0.733	12.8	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS11A/YDR025W	156	0.705	12.8	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS13/YDR064W	151	0.776	49.0	5 (5)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS14A/YCR031C	137	0.805	19.0	0 (3)	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS14B/YJL191W	138	0.59	18.8	↑	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS15/YOL040C	142	0.769	30.3	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS16B/YDL083C	143	0.764	20.3	0 (3)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	20.3	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	15.8	0 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	15.8	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	23.5	0 (7)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	28.2	1 (8)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	10.7	2 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	40.8	0 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	40.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS24A/YER074W	135	0.816	24.4	0 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS24B/YIL069C	135	0.756	24.4	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	31.2	5 (5)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS4B/YHR203C	261	0.709	36.4	0 (10)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	36.4	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	27.5	0 (5)	36.36 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS6A/YPL090C	236	0.837	27.5	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	8.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	8.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SRO9/YCL037C	466	0.264	13.9	5 (5)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	22.7	0 (12)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	33.2	2 (15)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	8.6	0 (6)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	11.5	0 (7)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	23.5	0 (10)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	23.5	↑	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	16.0	0 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	27.1	0 (7)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	45.5	2 (9)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	17.0	0 (7)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	17.0	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	9.3	12 (12)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
VMA2/YBR127C	517	0.39	15.9	5 (5)	22.73 %	H^+–exporting ATPase	vacuolar acidification
YAR009C	NF	NF	3.1	0 (3)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	2.1	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	3.2	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	10.5	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	10.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YDR261C-C	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	10.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	4.7	0 (7)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	4.7	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	4.7	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	4.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	4.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	4.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	4.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	5.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	4.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	6.4	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	3.7	0 (6)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	3.1	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	2.8	0 (4)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	2.8	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

11 TAP–MuDPIT analysis of immune precipitations with GLC7–HPM (YER133W) as the bait protein

Table 20: Previously reported interaction partners of GLC7 (YER133W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are:CIC1/YHR052W (G/Y, physical), MVD1/YNR043W (Y, physical), YCL046W (Y, physical), YHR100C (M/G/Y, physical),SPB1/YCL054W (G/Y, physical), UTP15/YMR093W (Y, physical), POP7/YBR167C (Y, physical), SPO21/YOL091W (Y, physical), TYE7/YOR344C (Y, physical), ADK1/YDR226W (Y, physical), PRE9/YGR135W (Y, physical), SEC21/YNL287W (Y, physical), YOR179C (G/Y, physical), YHL035C (Y, physical), UTP6/YDR449C (Y, physical), PMA1/YGL008C (Y, physical), IMP3/YHR148W (Y, physical), MCR1/YKL150W (Y, physical), ECM29/YHL030W (Y, physical), SIP5/YMR140W (Y, physical), RRP9/YPR137W (Y, physical), NOP6/YDL213C (Y, physical), FPR4/YLR449W (G/Y, physical), PWP2/YCR057C (Y, physical), RVB1/YDR190C (Y, physical), MGE1/YOR232W (Y, physical), HTA2/YBL003C (Y, physical), HRR25/YPL204W (GRID, physical), PFK1/YGR240C (Y, physical), SIK1/YLR197W (Y, physical), TIF4632/YGL049C (Y, physical), YDR412W (M/G/Y, physical), SEC13/YLR208W (Y, physical), FPR3/YML074C (G/Y, physical), KRE33/YNL132W (Y, physical), FUR1/YHR128W (Y, physical), YTH1/YPR107C (G/Y, physical), YGR130C (Y, physical), UTP20/YBL004W (Y, physical), RML2/YEL050C (Y, physical), CLP1/YOR250C (Y, physical), UTP21/YLR409C (Y, physical), UTP22/YGR090W (Y, physical), NOP14/YDL148C (Y, physical), GAC1/YOR178C (M/Y, gen./phys.), YBR099C (M/G/Y, physical), GIP2/YER054C (G/Y, physical), EMG1/YLR186W (Y, physical), ROK1/YGL171W (Y, physical), HHF2/YNL030W (Y, physical), PRE6/YOL038W (Y, physical), SPE3/YPR069C (Y, physical), KRR1/YCL059C (Y, physical), VAS1/YGR094W (Y, physical), RTG2/YGL252C (Y, physical), SOF1/YLL011W (Y, physical), SSZ1/YHR064C (Y, physical), TAF6/YGL112C (Y, physical), HMS1/YOR032C (Y, physical), SEC31/YDL195W (Y, physical), PRP43/YGL120C (Y, physical), UTP8/YGR128C (Y, physical), YOR315W (M/G/Y, gen./phys.), IPL1/YPL209C (M/Y, genetic), SLA1/YBL007C (Y, physical), CIN8/YEL061C (MIPS, genetic), NAN1/YPL126W (Y, physical), BUD21/YOR078W (Y, physical), ADH4/YGL256W (G/Y, physical), UTP10/YJL109C (Y, physical), PMA2/YPL036W (Y, physical), KOG1/YHR186C (Y, physical), HXT6/YDR343C (Y, physical), BMS1/YPL217C (Y, physical), UTP30/YKR060W (Y, physical), YTA6/YPL074W (Y, physical), GSY1/YFR015C (G/Y, physical), ENP1/YBR247C (Y, physical), PDC5/YLR134W (G/Y, physical), DAM1/YGR113W (Y, genetic), NET1/YJL076W (Y, physical), SYN8/YAL014C (Y, physical), NOP1/YDL014W (Y, physical), PFS2/YNL317W (Y, physical), MEK1/YOR351C (Y, physical), DPM1/YPR183W (Y, physical), YDL094C (Y, physical), RNA14/YMR061W (Y, physical), PAN1/YIR006C (M/G/Y, physical), MPP10/YJR002W (Y, physical), ATP3/YBR039W (Y, physical), CKA1/YIL035C (Y, physical), BFR2/YDR299W (Y, physical), DBP8/YHR169W (Y, physical), RSA3/YLR221C (Y, physical), ADE4/YMR300C (Y, physical), ENP2/YGR145W (Y, physical), UTP9/YHR196W (Y, physical), HTA1/YDR225W (Y, physical), GCN1/YGL195W (Y, physical), PHO85/YPL031C (Y, physical), UTP7/YER082C (Y, physical), TSA2/YDR453C (Y, physical), CDC2/YDL102W (Y, genetic), RSE1/YML049C (Y, physical), IMP4/YNL075W (Y, physical), TIF1/YKR059W (Y, physical), CFT2/YLR115W (G/Y, physical), ATP7/YKL016C (Y, physical), GSY2/YLR258W (G/Y, physical), DIP2/YLR129W (Y, physical), ERB1/YMR049C (G/Y, physical), CBF5/YLR175W (Y, physical), NSA1/YGL111W (G/Y, physical), HEF3/YNL014W (Y, physical), REG2/YBR050C (M/Y, physical), ECM16/YMR128W (Y, physical), CDC14/YFR028C (G/Y, physical), SUI2/YJR007W (G/Y, physical), VPS53/YJL029C (Y, physical), ATP5/YDR298C (Y, physical), UTP18/YJL069C (Y, physical), YTM1/YOR272W (GRID, physical), HCA4/YJL033W (G/Y, physical), NOP12/YOL041C (Y, physical), RNA15/YGL044C (Y, physical), PCF11/YDR228C (Y, physical), YSH1/YLR277C (G/Y, physical), YNR054C (Y, physical), VID24/YBR105C (Y, physical), SCL1/YGL011C (Y, physical), FIN1/YDR130C (M/G/Y, physical), GDB1/YPR184W (Y, physical), BDF2/YDL070W (M/G/Y, physical), BUD27/YFL023W (M/G/Y, physical), CLU1/YMR012W (G/Y, physical), NOC4/YPR144C (Y, physical), UTP11/YKL099C (Y, physical), YDR365C (Y, physical), NOP7/YGR103W (G/Y, physical), GPH1/YPR160W (G/Y, physical), UTP4/YDR324C (Y, physical), UTP13/YLR222C (Y, physical), TPS1/YBR126C (Y, physical), NOP58/YOR310C (Y, physical), ERO1/YML130C (Y, physical), SUI3/YPL237W (G/Y, physical), GIP1/YBR045C (M/G/Y, physical), MDH1/YKL085W (G/Y, physical), HSL1/YKL101W (Y, physical), HAS1/YMR290C (Y, physical), RED1/YLR263W (M/G/Y, physical), YML030W (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
GLC7/YER133W	Bait	Bait	312	0.229	94.6	103 (108)	13.64 %	protein phosphatase type 1*	meiosis*

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Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACT1/YFL039C	physical	Y	375	0.711	12.3	2 (2)	18.18 %	struct. const. of cytoskeleton	cell wall organ. and biogen.*
BNI4/YNL233W	physical	M/G/Y	892	0.138	43.2	35 (35)	4.55 %	protein binding	cytokinesis
BUD14/YAR014C	physical	M/G/Y	702	0.118	19.1	14 (14)	4.55 %	mol. funct. unknown	bud site selection*
CFT1/YDR301W	physical	G/Y	1357	0.153	5.7	4 (4)	4.55 %	cleav./polyadenyl. specif. fact.	mRNA polyadenylation*
ENO2/YHR174W	physical	Y	437	0.892	35.5	5 (12)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
FIP1/YJR093C	physical	G/Y	327	0.119	19.9	5 (5)	4.55 %	cleav./polyadenyl. specif. fact.	mRNA polyadenylation*
GLC8/YMR311C	physical	G/Y	229	0.122	67.2	28 (28)	4.55 %	enzyme activator	glycogen biosynthesis
KEL1/YHR158C	physical	G/Y	1164	0.142	2.9	2 (2)	9.09 %	mol. funct. unknown	cell. morphogenesis*
MHP1/YJL042W	physical	M/G/Y	1398	0.152	20.5	22 (22)	4.55 %	struct. const. of cytoskeleton	cell wall organ. and biogen.*
MPE1/YKL059C	physical	G/Y	441	0.149	10.2	3 (3)	4.55 %	mol. funct. unknown	mRNA polyadenylation*
NSR1/YGR159C	physical	Y	414	0.493	41.8	16 (16)	9.09 %	RNA binding*	rRNA processing*
PAP1/YKR002W	physical	G/Y	568	0.158	14.8	6 (6)	4.55 %	polynucleotide adenylyltransf.	mRNA polyadenylation
PPZ2/YDR436W	gen./phys.	Y	710	0.109	1.5	0 (5)	13.64 %	protein Ser/Thr phosphatase	sodium ion homeostasis
PPZ1/YML016C	gen./phys.	Y	692	0.164	1.6	↑	9.09 %	protein Ser/Thr phosphatase	sodium ion homeostasis
PTA1/YAL043C	physical	G/Y	785	0.13	7.4	3 (3)	4.55 %	cleav./polyadenyl. specif. fact.	mRNA polyadenylation*
PTI1/YGR156W	physical	Y	425	0.122	37.4	13 (13)	4.55 %	pre-mRNA cleavage factor	mRNA polyadenylation*
REF2/YDR195W	physical	M/G/Y	533	0.149	38.1	21 (21)	4.55 %	cleav./polyadenyl. specif. fact.	mRNA processing
REG1/YDR028C	gen./phys.	M/G/Y	1014	0.146	41.7	52 (52)	4.55 %	protein phosphatase type 1*	neg. regul. of Pol II prom. transcr.*
SCD5/YOR329C	physical	M/G/Y	872	0.13	15.9	10 (10)	4.55 %	protein binding	actin filament organization*
SDS22/YKL193C	physical	G/Y	338	0.182	85.8	85 (85)	13.64 %	enzyme regulator*	chromosome segregation*
SEN1/YLR430W	physical	G/Y	2231	0.15	1.4	2 (2)	4.55 %	ATP dep. RNA helicase	35S prim. transcript processing
SNF4/YGL115W	physical	Y	322	0.16	21.1	4 (4)	4.55 %	protein kinase activator	regul. of Pol II prom. transcr.*
SRO9/YCL037C	physical	Y	466	0.264	19.3	5 (5)	95.45 %	RNA binding	protein biosynthesis
SSA3/YBL075C	physical	Y	649	0.177	11.2	1 (6)	81.82 %	heat shock protein	response to stress*
SSU72/YNL222W	physical	Y	206	0.155	48.5	5 (5)	4.55 %	mol. funct. unknown	transcr. init. from Pol II prom.
SWD2/YKL018W	physical	Y	329	0.136	65.0	23 (23)	4.55 %	histone–Lys N–methyltransf.	histone methylation
YOR227W	physical	G/Y	1246	0.149	14.4	12 (12)	4.55 %	mol. funct. unknown	biological process unknown
YPI1/YFR003C	physical	G/Y	155	0.121	63.9	20 (20)	13.64 %	mol. funct. unknown	biological process unknown

Table 21: Potential interactors recovered through TAP–MuDPIT on GLC7/YER133W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ABF1/YKL112W	731	0.178	2.2	2 (2)	4.55 %	transcr. factor*	chromatin silencing at HML and HMR*
ADE16/YLR028C	591	0.173	35.2	9 (12)	9.09 %	IMP cyclohydrolase*	aerobic respiration*
ADE17/YMR120C	592	0.322	6.9	0 (3)	4.55 %	IMP cyclohydrolase*	'de novo' IMP biosynthesis
AHP1/YLR109W	176	0.549	21.0	2 (2)	9.09 %	thioredoxin peroxidase	regulation of redox homeostasis*
BMH1/YER177W	267	0.323	72.3	6 (30)	18.18 %	DNA binding	pseudohyphal growth*
BMH2/YDR099W	273	0.385	71.1	7 (31)	9.09 %	DNA binding	pseudohyphal growth*
CCR4/YAL021C	837	0.137	4.9	3 (3)	4.55 %	3'-5' exoribonuclease	regul. of Pol II prom. transcr.*
CKA2/YOR061W	339	0.164	10.0	3 (3)	4.55 %	protein kinase CK2	prot. AA phosphoryl.*
ENO1/YGR254W	437	0.871	28.1	2 (9)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
FUN21/YAL031C	760	0.123	4.2	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
GAL83/YER027C	417	0.141	8.2	3 (3)	4.55 %	SNF1A/AMP-activ. prot. kinase	prot. AA phosphoryl.*
HSP60/YLR259C	572	0.382	7.5	3 (3)	13.64 %	heat shock protein	protein folding*
IMP2'/YIL154C	346	0.109	15.0	3 (3)	4.55 %	transcr. co-activator	DNA repair*
MOR1/YOL063C	957	0.131	6.8	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
PDC1/YLR044C	563	0.904	10.8	4 (5)	18.18 %	pyruvate decarboxylase	pyruvate metabolism*
PGK1/YCR012W	416	0.815	28.8	7 (7)	18.18 %	phosphoglycerate kinase	gluconeogenesis*
POL2/YNL262W	2222	0.146	1.7	2 (2)	4.55 %	epsilon DNA polymerase	lagging strand elongation*
RPP2A/YOL039W	106	0.804	29.2	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis*
SNF1/YDR477W	633	0.188	11.4	5 (5)	18.18 %	SNF1A/AMP-activ. prot. kinase	prot. AA phosphoryl.*
SOL1/YNR034W	321	0.121	15.0	2 (3)	4.55 %	mol. funct. unknown	tRNA processing
SOL2/YCR073W-A	315	0.116	14.6	2 (3)	4.55 %	mol. funct. unknown	tRNA processing
YBR225W	900	0.141	3.8	2 (2)	9.09 %	mol. funct. unknown	biological process unknown
YDR474C	555	0.122	9.9	3 (3)	4.55 %	mol. funct. unknown	biological process unknown
YER158C	573	0.129	11.0	4 (4)	4.55 %	mol. funct. unknown	biological process unknown
YGR237C	785	0.14	20.3	13 (13)	4.55 %	mol. funct. unknown	biological process unknown
YHR097C	366	0.125	13.4	3 (3)	9.09 %	mol. funct. unknown	biological process unknown
YPL137C	1276	0.164	25.8	27 (27)	9.09 %	mol. funct. unknown	biological process unknown

Table 22: Proteins which co–purify with GLC7/YER133W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	34.2	7 (9)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	9.5	1 (3)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	12.3	2 (3)	50.00 %	alcohol dehydrogenase	fermentation
CDC19/YAL038W	500	0.893	21.0	9 (9)	50.00 %	pyruvate kinase	glycolysis*
FBA1/YKL060C	359	0.869	26.7	7 (7)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HSC82/YMR186W	705	0.581	4.0	0 (2)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	3.9	↑	27.27 %	chaperonin ATPase	response to stress*
HYP2/YEL034W	157	0.814	7.6	2 (2)	27.27 %	translation initiation factor	translational initiation
KCS1/YDR017C	1050	0.144	4.4	3 (3)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	5.8	3 (3)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	26.6	8 (8)	95.45 %	mRNA binding	mRNA-nucleus export
RPL15A/YLR029C	204	0.783	20.6	0 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	20.6	↑	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL1B/YGL135W	217	0.832	18.4	0 (4)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	18.4	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	15.5	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	28.7	0 (3)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	28.7	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	18.9	0 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	18.9	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	7.5	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	7.5	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL8A/YHL033C	256	0.842	20.7	0 (3)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	20.7	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	16.2	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS6B/YBR181C	236	0.846	11.4	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	11.4	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	27.3	14 (14)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA1/YAL005C	642	0.709	22.7	1 (10)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	18.0	0 (9)	100.00 %	heat shock protein	protein folding*
SSA4/YER103W	642	0.184	7.2	0 (4)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	38.8	1 (20)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	38.8	↑	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	23.5	2 (7)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	23.5	0 (7)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	45.2	5 (12)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	11.4	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	11.4	↑	90.91 %	translation elongation factor	translational elongation
UGP1/YKL035W	499	0.33	23.8	7 (7)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*

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Table 23: Previously reported interaction partners of INO4 (YOL108C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: LYS12/YIL094C (Y, physical), BLM3/YFL007W (Y, physical), RTG1/YOL067C (Y, physical), PRE4/YFR050C (Y, physical), PSE1/YMR308C (G/Y, physical), DAM1/YGR113W (Y, physical), GFA1/YKL104C (Y, physical), PRM1/YNL279W (M/G/Y, physical), YLR422W (Y, physical), DBP9/YLR276C (Y, physical), YGR081C (Y, physical), YMR310C (Y, physical), ECM29/YHL030W (Y, physical), RTG3/YBL103C (Y, physical), MDS3/YGL197W (Y, physical), RPT5/YOR117W (Y, physical), PRE3/YJL001W (Y, physical), RRP12/YPL012W (Y, physical), HTB2/YBL002W (G/Y, physical), RGR1/YLR071C (Y, physical), PUP3/YER094C (Y, physical), PRE5/YMR314W (Y, physical), EST3/YIL009C-A (Y, physical), APL2/YKL135C (M/G/Y, physical), PDA1/YER178W (Y, physical), PDB1/YBR221C (Y, physical), RPT3/YDR394W (Y, physical), PRE9/YGR135W (Y, physical), YRA1/YDR381W (Y, physical), SRP1/YNL189W (Y, physical), YFL006W (Y, physical), BCK2/YER167W (Y, physical), NIP7/YPL211W (G/Y, physical), NUD1/YOR373W (Y, physical), SCL1/YGL011C (Y, physical), TYE7/YOR344C (Y, physical), PRE2/YPR103W (Y, physical), PRE6/YOL038W (Y, physical), MAM33/YIL070C (G/Y, physical), KAP95/YLR347C (Y, physical), PHO4/YFR034C (Y, physical), UTP4/YDR324C (G/Y, physical), PRE8/YML092C (Y, physical), ULP1/YPL020C (Y, physical), YNR064C (Y, physical), HCS1/YKL017C (M/G/Y, physical), SPA2/YLL021W (Y, physical), HHF1/YBR009C (G/Y, physical), PRE10/YOR362C (Y, physical), YMR317W (M/G/Y, physical), HTB1/YDR224C (G/Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
INO4/YOL108C	Bait	Bait	151	0.083	49.0	7 (7)	4.55 %	spec. pol II transcr. fact.	pos. regul. of Pol II prom. transcr.*
INO2/YDR123C	physical	M/G/Y	304	0.123	24.7	4 (4)	4.55 %	spec. pol II transcr. fact.	pos. regul. of Pol II prom. transcr.*

Table 24: Potential interactors recovered through TAP–MuDPIT on INO4/YOL108C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACT1/YFL039C	375	0.711	15.7	5 (5)	18.18 %	struct. const. of cytoskeleton	cell wall organ. and biogen.*
MDN1/YLR106C	4910	0.161	0.5	2 (2)	4.55 %	ATPase	protein complex assembly
PMD1/YER132C	1753	0.12	2.4	2 (2)	4.55 %	mol. funct. unknown	sporulation
XRS2/YDR369C	854	0.14	3.6	2 (2)	4.55 %	protein binding	DSB repair by nonhomol. end–joining*

Table 25: Proteins which co–purify with INO4/YOL108C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
FBA1/YKL060C	359	0.869	13.1	3 (3)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HSC82/YMR186W	705	0.581	3.7	0 (2)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	3.7	↑	27.27 %	chaperonin ATPase	response to stress*
KAR2/YJL034W	682	0.44	4.3	0 (2)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
NPL3/YDR432W	414	0.359	14.7	5 (5)	95.45 %	mRNA binding	mRNA-nucleus export
RPL28/YGL103W	149	0.705	39.6	6 (6)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	26.8	0 (3)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	26.8	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL31A/YDL075W	113	0.737	24.8	0 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	24.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	13.1	0 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	13.1	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	13.0	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	13.0	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	14.5	2 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	13.8	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	13.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	16.2	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS4B/YHR203C	261	0.709	11.5	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.5	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SRO9/YCL037C	466	0.264	7.9	2 (2)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	6.7	0 (4)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	6.7	↑	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	7.2	0 (5)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	9.2	0 (6)	72.73 %	chaperone*	response to stress*
TDH1/YJL052W	332	0.856	13.0	1 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	17.2	0 (4)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	19.3	1 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
TEF2/YBR118W	458	0.876	7.6	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	7.6	↑	90.91 %	translation elongation factor	translational elongation
UGP1/YKL035W	499	0.33	13.0	5 (5)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
YBR012W-B	NF	NF	2.1	0 (2)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	2.1	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	2.1	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	2.1	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	2.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	2.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	2.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	2.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	2.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	2.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Table 26: Previously reported interaction partners of LTE1 (YAL024C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: TEM1/YML064C (M/G/Y, gen./phys.), PRE7/YBL041W (Y, physical), CDC55/YGL190C (Y, physical), ERG13/YML126C (Y, physical), BLM3/YFL007W (Y, physical), PRE4/YFR050C (Y, physical), TPD3/YAL016W (G/Y, physical), PRE9/YGR135W (Y, physical), KEL2/YGR238C (Y, physical), SNT1/YCR033W (Y, physical), CDC24/YAL041W (Y, genetic), PRE1/YER012W (Y, physical), CDC15/YAR019C (MIPS, genetic), PUP1/YOR157C (Y, physical), SIF2/YBR103W (Y, physical), RSR1/YGR152C (M/G, genetic), PRE8/YML092C (Y, physical), YOR1/YGR281W (Y, physical), CIN1/YOR349W (Y, physical), PPH22/YDL188C (Y, physical), ZDS2/YML109W (Y, physical), PUP3/YER094C (Y, physical), ZDS1/YMR273C (Y, physical), RAS1/YOR101W (M/G, genetic), SPO12/YHR152W (MIPS, genetic), HHF2/YNL030W (Y, physical), STE20/YHL007C (Y, genetic), ESP1/YGR098C (Y, genetic), CDC42/YLR229C (Y, genetic), HOS4/YIL112W (Y, physical), YRA1/YDR381W (Y, physical), PRE5/YMR314W (Y, physical), SRP1/YNL189W (Y, physical), IRA1/YBR140C (MIPS, genetic), SET3/YKR029C (Y, physical), RTS3/YGR161C (Y, physical), MOB1/YIL106W (M/G/Y, genetic), YBL104C (Y, physical), RRD2/YPL152W (Y, physical), SCL1/YGL011C (Y, physical), RTS1/YOR014W (Y, physical), MSL1/YIR009W (M/G, physical), MYO5/YMR109W (Y, physical), PRE2/YPR103W (Y, physical), PRE6/YOL038W (Y, physical), IML1/YJR138W (Y, physical), TEF4/YKL081W (Y, physical), KAP95/YLR347C (Y, physical), RAS2/YNL098C (M/G, genetic), PUP2/YGR253C (Y, physical), YGL245W (Y, physical), HOS2/YGL194C (Y, physical), PPH21/YDL134C (Y, physical), PRE10/YOR362C (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
LTE1/YAL024C	Bait	Bait	1435	0.123	48.6	76 (76)	4.55 %	guanyl-nucleotide exchange factor	regul. of exit from mitosis
KEL1/YHR158C	physical	G/Y	1164	0.142	23.7	19 (19)	9.09 %	mol. funct. unknown	cell. morphogenesis*
PFK1/YGR240C	physical	Y	987	0.466	8.9	6 (6)	63.64 %	6-phosphofructokinase	glycolysis
TDH2/YJR009C	physical	Y	332	0.905	49.4	0 (20)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	physical	Y	332	0.924	84.9	18 (36)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
YEF3/YLR249W	physical	Y	1044	0.778	34.8	23 (27)	54.55 %	translation elongation factor	translational elongation

Table 27: Potential interactors recovered through TAP–MuDPIT on LTE1/YAL024C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADE4/YMR300C	510	0.235	7.6	3 (3)	4.55 %	amidophosphoribosyltransferase	purine base metabolism
ARO2/YGL148W	376	0.323	7.2	2 (2)	9.09 %	chorismate synthase	aromatic AA family biosynthesis
ASC1/YMR116C	319	0.777	9.4	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
ASN1/YPR145W	572	0.368	4.7	0 (2)	9.09 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
BCY1/YIL033C	416	0.178	7.5	2 (2)	9.09 %	cAMP-dep. protein kinase inhibitor	response to stress*
BMH1/YER177W	267	0.323	10.1	1 (2)	18.18 %	DNA binding	pseudohyphal growth*
CAF20/YOR276W	161	0.356	28.0	2 (2)	18.18 %	translation regulator	negative regulation of translation
CAR2/YLR438W	424	0.292	11.1	3 (3)	13.64 %	ornithine-oxo-acid aminotransferase	arginine catabolism
CDC33/YOL139C	213	0.387	14.1	3 (3)	13.64 %	translation initiation factor	translational initiation*
EFT2/YDR385W	842	0.8	4.0	0 (2)	18.18 %	translation elongation factor	translational elongation
EFT1/YOR133W	842	0.804	4.0	↑	18.18 %	translation elongation factor	translational elongation
EMI2/YDR516C	500	0.178	10.4	4 (4)	9.09 %	mol. funct. unknown	biological process unknown
ENO1/YGR254W	437	0.871	17.4	2 (6)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
ENO2/YHR174W	437	0.892	29.1	5 (9)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
FLO8/YER109C	798	0.104	1.0	2 (2)	4.55 %	spec. pol II transcr. fact.	pseudohyphal growth*
GAD1/YMR250W	585	0.171	4.1	2 (2)	4.55 %	glutamate decarboxylase	response to oxidative stress*
GLK1/YCL040W	500	0.158	17.0	5 (5)	9.09 %	glucokinase	carbohydrate metabolism
GLT1/YDL171C	2145	0.287	4.8	6 (6)	13.64 %	glutamate synthase (NADH)	glutamate biosynthesis
GLY1/YEL046C	387	0.33	11.9	3 (3)	18.18 %	threonine aldolase	threonine catabolism*
GPM1/YKL152C	247	0.811	9.3	2 (2)	9.09 %	phosphoglycerate mutase	gluconeogenesis*
GUA1/YMR217W	525	0.462	7.8	3 (3)	9.09 %	GMP synthase (Glu hydrolyzing)	GMP metabolism
HEF3/YNL014W	1044	0.169	5.0	1 (5)	18.18 %	ATPase*	translational elongation
HEM1/YDR232W	548	0.213	5.7	2 (2)	4.55 %	5-aminolevulinate synthase	heme biosynthesis
HSP60/YLR259C	572	0.382	4.4	2 (2)	13.64 %	heat shock protein	protein folding*
ILV6/YCL009C	309	0.242	14.2	3 (3)	13.64 %	enzyme regulator*	branched chain family AA biosynth.
LPD1/YFL018C	499	0.253	6.6	2 (2)	4.55 %	dihydrolipoamide dehydrogenase	serine biosynthesis*
MKT1/YNL085W	830	0.203	3.7	2 (2)	9.09 %	mol. funct. unknown	viral life cycle
NFS1/YCL017C	497	0.226	6.2	2 (2)	18.18 %	cysteine desulfhydrase	iron ion homeostasis*
PBI2/YNL015W	75	0.371	41.3	4 (4)	4.55 %	endopeptidase inhibitor	vacuole fusion (non-autophagic)*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PDC1/YLR044C	563	0.904	15.6	6 (6)	18.18 %	pyruvate decarboxylase	pyruvate metabolism*
PGK1/YCR012W	416	0.815	26.0	8 (8)	18.18 %	phosphoglycerate kinase	gluconeogenesis*
PNC1/YGL037C	216	0.319	25.9	6 (6)	18.18 %	nicotinamidase	chromatin silencing at telomere*
PRO1/YDR300C	428	0.198	8.4	2 (2)	9.09 %	glutamate 5-kinase	proline biosynthesis
RAX2/YLR084C	1220	0.122	2.6	2 (2)	4.55 %	mol. funct. unknown	bud site selection
RIB4/YOL143C	169	0.211	28.4	4 (4)	13.64 %	6,7-dimethyl-8-ribityllumazine synthase	vitamin B2 biosynthesis
RPL23A/YBL087C	137	0.624	27.7	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL23B/YER117W	137	0.648	27.7	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPS23A/YGR118W	145	0.726	12.4	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS23B/YPR132W	145	0.789	12.4	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS29A/YLR388W	56	0.653	33.9	2 (3)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS29B/YDL061C	56	0.76	33.9	1 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPS5/YJR123W	225	0.838	12.4	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
SEC23/YPR181C	768	0.229	15.5	8 (8)	18.18 %	GTPase activator	ER to Golgi transport*
SEC24/YIL109C	926	0.212	5.0	3 (3)	4.55 %	protein binding	ER to Golgi transport*
SHM2/YLR058C	469	0.589	20.0	7 (7)	13.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SOD1/YJR104C	154	0.377	24.7	2 (2)	4.55 %	copper, zinc superoxide dismutase	zinc ion homeostasis*
TPI1/YDR050C	248	0.817	9.3	2 (2)	4.55 %	triose–P_i isomerase	gluconeogenesis*
TPS3/YMR261C	1054	0.202	9.4	6 (6)	4.55 %	α,α-trehalose–P_i synthase (UDP-forming)	response to stress*
VPS1/YKR001C	704	0.249	5.5	3 (3)	9.09 %	GTPase	protein-vacuolar targeting*
YDR348C	499	0.146	6.8	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
YHB1/YGR234W	399	0.267	8.5	2 (2)	18.18 %	mol. funct. unknown	response to stress
YHL021C	465	0.163	8.2	2 (2)	4.55 %	mol. funct. unknown	biological process unknown

Table 28: Proteins which co–purify with LTE1/YAL024C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	31.5	15 (16)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	54.3	13 (17)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	15.8	2 (6)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	20.3	5 (5)	50.00 %	alcohol dehydrogenase	fermentation
ASN2/YGR124W	572	0.317	21.0	6 (8)	22.73 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
CDC19/YAL038W	500	0.893	12.6	5 (6)	50.00 %	pyruvate kinase	glycolysis*
CLU1/YMR012W	1277	0.227	2.1	2 (2)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	4.1	2 (2)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	36.8	10 (10)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HYP2/YEL034W	157	0.814	19.1	4 (4)	27.27 %	translation initiation factor	translational initiation
ILV1/YER086W	576	0.312	16.8	5 (5)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
MIS1/YBR084W	975	0.208	3.4	2 (3)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	23.9	6 (6)	95.45 %	mRNA binding	mRNA-nucleus export
PFK2/YMR205C	959	0.512	6.7	6 (6)	31.82 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	6.5	4 (4)	31.82 %	serine-type endopeptidase	sporulation*
PSA1/YDL055C	361	0.6	13.3	3 (3)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL10/YLR075W	221	0.827	7.7	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL15A/YLR029C	204	0.783	17.2	1 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	13.7	0 (2)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL17B/YJL177W	184	0.68	28.8	0 (3)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	184	0.809	28.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	14.3	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	14.3	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	18.3	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL28/YGL103W	149	0.705	30.2	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	31.1	0 (7)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	31.1	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	5.4	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL31A/YDL075W	113	0.737	57.5	1 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	49.6	0 (5)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL40A/YIL148W	128	0.742	17.2	1 (2)	18.18 %	struct. const. of ribosome*	protein biosynthesis*
UBI4/YLL039C	381	0.317	5.8	↑	22.73 %	protein tagging*	response to stress*
RPL40B/YKR094C	128	0.742	17.2	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis*
RPL4A/YBR031W	362	0.803	26.2	1 (6)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	26.2	1 (6)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6B/YLR448W	176	0.627	13.1	0 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL6A/YML073C	176	0.672	13.1	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	12.1	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	12.1	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	17.8	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	17.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	9.9	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS15/YOL040C	142	0.769	22.5	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	11.4	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	11.4	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	27.3	4 (4)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	36.2	0 (5)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	36.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS31/YLR167W	152	0.811	34.9	3 (4)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPS4B/YHR203C	261	0.709	11.5	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.5	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	15.7	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	15.7	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	17.0	6 (6)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	19.1	6 (6)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	5.9	1 (3)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	6.3	1 (3)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	3.5	1 (2)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	3.7	0 (2)	72.73 %	chaperone*	response to stress*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSB1/YDL229W	613	0.82	5.2	1 (3)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	5.2	↑	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	6.8	4 (4)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	51.5	7 (16)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	38.6	0 (17)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	38.6	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	17.6	12 (12)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
TRP5/YGL026C	707	0.32	24.0	10 (10)	22.73 %	tryptophan synthase	tryptophan biosynthesis
UGP1/YKL035W	499	0.33	42.1	16 (16)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	2.1	4 (4)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	2.5	0 (2)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161W-B	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YFL002W-A	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210W-B	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR034C-D	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YCL019W	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL101W-B	NF	NF	1.7	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	22.3	0 (6)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	22.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	22.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	22.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	22.3	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	3.2	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	17.5	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	17.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	17.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	17.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	17.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	6.8	0 (7)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	6.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	7.7	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	7.7	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YDR210C-C	NF	NF	13.0	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	6.6	0 (7)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	8.7	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	7.7	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	8.9	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	8.9	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	8.0	0 (8)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	3.5	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	3.2	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	3.7	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	3.7	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	3.7	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	3.7	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	2.8	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	2.5	0 (2)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YNL054W-B	NF	NF	2.5	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Table 29: Previously reported interaction partners of MAD2 (YJL030W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: SIN4/YNL236W (M/G/Y, physical), CEP3/YMR168C (Y, genetic), KAR3/YPR141C (M/G/Y, genetic), BET2/YPR176C (Y, genetic), MAD3/YJL013C (Y, physical), NUP157/YER105C (M/G/Y, physical), EBS1/YDR206W (M/G/Y, physical), BIM1/YER016W–HPM (M/G/Y, genetic), CTF19/YPL018W (Y, genetic), GLO3/YER122C (GRID, physical), AHA1/YDR214W (M/G/Y, physical), DAM1/YGR113W (Y, genetic), MSB2/YGR014W (M/G/Y, physical), SKP1/YDR328C (Y, genetic), MGS1/YNL218W (M/G/Y, physical), SAP4/YGL229C (M/G/Y, physical), CIN8/YEL061C (M/G/Y, genetic), MCM21/YDR318W (Y, genetic), CTF13/YMR094W (Y, genetic);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
MAD2/YJL030W	Bait	Bait	196	0.115	84.7	72 (72)	9.09 %	mol. funct. unknown	mit. spindle checkpoint
CDC20/YGL116W	physical	M/G/Y	610	0.14	7.2	2 (2)	9.09 %	enzyme activator	ubiquitin–dep. prot. catabol.*
MAD1/YGL086W	physical	Y	749	0.142	66.1	113 (114)	4.55 %	mol. funct. unknown	mit. spindle checkpoint*

Table 30: Potential interactors recovered through TAP–MuDPIT on MAD2/YJL030W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
APL4/YPR029C	832	0.149	3.4	2 (2)	4.55 %	clathrin binding	vesicle-mediated transport
CAF20/YOR276W	161	0.356	17.4	2 (2)	18.18 %	translation regulator	negative regulation of translation
ENO1/YGR254W	437	0.871	12.1	1 (4)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
ENO2/YHR174W	437	0.892	21.3	5 (8)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
PDC1/YLR044C	563	0.904	8.3	2 (3)	18.18 %	pyruvate decarboxylase	pyruvate metabolism*
PGK1/YCR012W	416	0.815	21.2	6 (6)	18.18 %	phosphoglycerate kinase	gluconeogenesis*
RRB1/YMR131C	511	0.209	5.3	2 (2)	13.64 %	mol. funct. unknown	ribosome biogenesis
TRX2/YGR209C	104	0.425	35.6	2 (3)	9.09 %	thiol-disulfide exchange intermediate	response to oxidative stress*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
URA7/YBL039C	579	0.309	3.8	1 (2)	13.64 %	CTP synthase	phospholipid biosynthesis*
YOR283W	230	0.233	13.9	2 (2)	4.55 %	mol. funct. unknown	biological process unknown

Table 31: Proteins which co–purify with MAD2/YJL030W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	12.3	4 (5)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	43.7	10 (15)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	25.6	2 (7)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	5.1	0 (2)	50.00 %	alcohol dehydrogenase	fermentation
CDC19/YAL038W	500	0.893	8.0	2 (3)	50.00 %	pyruvate kinase	glycolysis*
CLU1/YMR012W	1277	0.227	3.9	3 (3)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	10.2	3 (3)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	14.5	3 (3)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HYP2/YEL034W	157	0.814	16.6	1 (2)	27.27 %	translation initiation factor	translational initiation
KCS1/YDR017C	1050	0.144	4.1	4 (4)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	3.8	2 (3)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	20.0	8 (8)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	2.6	2 (2)	63.64 %	6-phosphofructokinase	glycolysis
RPL31A/YDL075W	113	0.737	22.1	1 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	34.0	1 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	34.0	1 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	29.2	0 (4)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	29.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	5.7	3 (3)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	10.9	3 (3)	95.45 %	RNA binding	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA1/YAL005C	642	0.709	18.7	2 (9)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	20.7	3 (10)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
TDH1/YJL052W	332	0.856	24.7	0 (6)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	40.1	1 (10)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	44.0	2 (12)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	14.0	0 (6)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	14.0	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	3.2	2 (2)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
UGP1/YKL035W	499	0.33	17.6	7 (7)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
YAR009C	NF	NF	1.9	0 (2)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	1.3	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	2.0	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	1.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	13.0	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	13.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	4.6	0 (6)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	4.6	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YGR027W-B	NF	NF	4.6	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	4.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	4.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	4.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	4.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	5.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	4.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	8.9	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	3.5	0 (5)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	3.7	2 (3)	54.55 %	translation elongation factor	translational elongation
YGR161C-D	NF	NF	2.3	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

15 TAP–MuDPIT analysis of immune precipitations with MCD1–HPM (YDL003W) as the bait protein

Table 32: Previously reported interaction partners of MCD1 (YDL003W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: RVB2/YPL235W (Y, physical), ESP1/YGR098C (Y, physical), CCT8/YJL008C (Y, physical), POL2/YNL262W (Y, genetic), YHB1/YGR234W (Y, physical), CDC20/YGL116W (Y, genetic), GCN1/YGL195W (Y, physical), CTF8/YHR191C (Y, genetic), SPC72/YAL047C (Y, physical), PDS5/YMR076C (Y, genetic), CDC28/YBR160W (Y, genetic), NOP12/YOL041C (Y, physical), KAP123/YER110C (Y, physical), SRP1/YNL189W (Y, physical), NOP13/YNL175C (Y, physical), HHF2/YNL030W (Y, physical), SCC4/YER147C (G/Y, physical), KAP95/YLR347C (Y, physical), IVY1/YDR229W (Y, physical), IRR1/YIL026C (G/Y, physical), DCC1/YCL016C (Y, genetic);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
MCD1/YDL003W	Bait	Bait	566	0.136	55.3	39 (39)	9.09 %	mol. funct. unknown	mit. chromosome condensation*
CDC5/YMR001C	physical	G/Y	705	0.166	10.9	7 (7)	4.55 %	prot. Ser/Thr kin.	prot. AA phosphoryl.*
SMC1/YFL008W	gen./phys.	M/G/Y	1225	0.163	70.9	134 (134)	4.55 %	ATPase*	mitotic chromosome segregation
SMC3/YJL074C	physical	M/G/Y	1230	0.181	67.8	133 (134)	4.55 %	ATPase	sporulation*
TRF4/YOL115W	genetic	Y	584	0.148	1.7	2 (2)	4.55 %	DNA–directed DNA pol.	mit. chromosome condensation*

Table 33: Potential interactors recovered through TAP–MuDPIT on MCD1/YDL003W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
BDF1/YLR399C	686	0.127	1.0	2 (2)	4.55 %	transcr. regulator	sporulation
CSM1/YCR086W	190	0.087	3.7	2 (2)	4.55 %	mol. funct. unknown	meiotic chromosome segregation
NUF2/YOL069W	451	0.139	1.6	↑	4.55 %	struct. const. of cytoskeleton	chromosome segregation*
NOT5/YPR072W	560	0.163	1.2	2 (2)	4.55 %	3'-5' exoribonuclease	regul. of Pol II prom. transcr.*
POM152/YMR129W	1337	0.157	2.2	2 (2)	4.55 %	struct. molecule	mRNA-nucleus export*
SRM1/YGL097W	482	0.204	8.9	4 (4)	9.09 %	signal transducer	rRNA-nucleus export*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
STU2/YLR045C	888	0.128	0.9	2 (2)	4.55 %	struct. const. of cytoskeleton*	microtubule nucleation*
YBL005W-A	NF	NF	8.2	0 (3)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR170W-A	NF	NF	8.2	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR045C	NF	NF	1.4	0 (2)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YNL284C-B	NF	NF	1.4	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YNL284C-A	NF	NF	5.5	↑	4.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR046C	NF	NF	5.5	↑	4.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 34: Proteins which co–purify with MCD1/YDL003W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	11.8	4 (4)	86.36 %	alcohol dehydrogenase	fermentation
CTS2/YDR371W	511	0.137	16.8	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
HOS3/YPL116W	697	0.157	26.3	11 (11)	22.73 %	histone deacetylase	histone deacetylation
HSC82/YMR186W	705	0.581	3.3	0 (2)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	3.2	↑	27.27 %	chaperonin ATPase	response to stress*
IMD2/YHR216W	523	0.305	6.3	0 (2)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD4/YML056C	524	0.471	6.3	↑	9.09 %	IMP dehydrogenase	biological process unknown
IMD3/YLR432W	523	0.464	6.3	↑	27.27 %	IMP dehydrogenase	GTP biosynthesis
MIS1/YBR084W	975	0.208	8.0	5 (5)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	20.0	7 (7)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	5.0	3 (3)	63.64 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	7.6	3 (3)	31.82 %	serine-type endopeptidase	sporulation*
RPL10/YLR075W	221	0.827	24.9	3 (3)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL17B/YJL177W	184	0.68	15.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	184	0.809	15.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL18B/YNL301C	186	0.68	14.5	0 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	14.5	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	10.6	0 (3)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	10.6	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	22.2	0 (4)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	23.0	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	30.2	5 (5)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	24.8	0 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	24.8	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL31A/YDL075W	113	0.737	39.8	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	39.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	18.8	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	18.8	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	16.2	0 (5)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	16.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	9.0	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS13/YDR064W	151	0.776	23.8	3 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS15/YOL040C	142	0.769	30.3	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	23.3	0 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	23.3	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	6.7	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	6.7	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	41.5	0 (8)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	41.5	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	16.7	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS4B/YHR203C	261	0.709	11.9	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.9	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	10.1	3 (3)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	6.7	2 (2)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	17.0	0 (8)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	17.1	↑	100.00 %	heat shock protein	protein folding*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA3/YBL075C	649	0.177	6.9	0 (3)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	6.2	0 (3)	72.73 %	chaperone*	response to stress*
TDH1/YJL052W	332	0.856	18.7	1 (4)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	19.6	0 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	19.6	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	19.0	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	19.0	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	2.1	2 (2)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	4.3	0 (4)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	3.0	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.5	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	2.9	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	3.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	18.0	0 (7)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	18.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	5.0	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	16.6	0 (6)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	16.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	16.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	16.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	16.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	7.1	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	7.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	7.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	7.1	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	7.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	8.2	0 (11)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	7.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	7.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YGR027W-B	NF	NF	6.8	0 (10)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	13.9	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	6.4	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	4.2	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	4.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	4.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	4.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	4.2	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

16 TAP–MuDPIT analysis of immune precipitations with PDS1–HPM (YDR113C) as the bait protein

Table 35: Previously reported interaction partners of PDS1 (YDR113C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: CDC20/YGL116W (Y, physical), NUP84/YDL116W (M/G/Y, physical), CHK1/YBR274W (Y, physical), SRP1/YNL189W (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PDS1/YDR113C	Bait	Bait	373	0.131	63.0	31 (31)	4.55 %	protein binding	protein-nucleus import*
ESP1/YGR098C	gen./phys.	M/G/Y	1630	0.113	14.8	23 (23)	4.55 %	cysteine-type endopeptidase	regul. of exit from mitosis*

Table 36: Potential interactors recovered through TAP–MuDPIT on PDS1/YDR113C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
AZR1/YGR224W	613	0.138	2.0	2 (2)	9.09 %	transporter	transport
IRE1/YHR079C	1115	0.116	4.0	2 (2)	4.55 %	prot. Ser/Thr kin.*	prot. AA phosphoryl.*
MSS1/YMR023C	526	0.117	7.0	2 (2)	9.09 %	GTP binding	protein biosynthesis
SWI3/YJL176C	825	0.148	3.9	2 (2)	13.64 %	gen. pol II transcr. fact.	chromatin modeling

Table 37: Proteins which co–purify with PDS1/YDR113C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	12.9	3 (4)	86.36 %	alcohol dehydrogenase	fermentation
CTS2/YDR371W	511	0.137	12.3	4 (4)	81.82 %	mol. funct. unknown	biological process unknown
KAR2/YJL034W	682	0.44	17.2	0 (9)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
MIS1/YBR084W	975	0.208	5.9	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	24.9	9 (9)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	7.3	4 (4)	63.64 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	7.6	3 (3)	31.82 %	serine-type endopeptidase	sporulation*
RPL20A/YMR242C	180	0.665	23.3	0 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	24.1	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	18.3	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL28/YGL103W	149	0.705	20.1	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	31.1	0 (6)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	31.1	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL31A/YDL075W	113	0.737	38.9	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	38.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	14.4	1 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	9.9	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	34.0	1 (7)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	34.0	1 (7)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	15.8	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	15.8	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	46.2	0 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	46.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS4B/YHR203C	261	0.709	16.1	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	16.1	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	12.4	4 (4)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	11.6	3 (3)	95.45 %	RNA binding	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA1/YAL005C	642	0.709	33.6	4 (19)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	37.6	4 (21)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	9.9	0 (6)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	12.9	0 (8)	72.73 %	chaperone*	response to stress*
TDH3/YGR192C	332	0.924	12.7	0 (3)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	12.7	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*

17 TAP–MuDPIT analysis of immune precipitations with PDS5–HPM (YMR076C) as the bait protein

Table 38: Previously reported interaction partners of PDS5 (YMR076C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PDS5/YMR076C	Bait	Bait	1277	0.162	52.8	100 (101)	4.55 %	struct. molecule	mit. chromosome condensation*
MCD1/YDL003W	genetic	Y	566	0.136	5.7	2 (2)	9.09 %	mol. funct. unknown	mit. chromosome condensation*

Table 39: Potential interactors recovered through TAP–MuDPIT on PDS5/YMR076C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ARO4/YBR249C	370	0.527	10.5	2 (2)	13.64 %	deoxyphosphoheptonate aldolase	aromatic AA family biosynthesis
CHS5/YLR330W	671	0.152	4.8	2 (2)	13.64 %	mol. funct. unknown	conjug. with cell. fusion*
HAL5/YJL165C	855	0.133	4.9	2 (2)	4.55 %	protein kinase	cation homeostasis
KEM1/YGL173C	1528	0.194	2.2	2 (2)	13.64 %	recombinase*	35S prim. transcript processing*
MSS1/YMR023C	526	0.117	4.2	1 (1)	9.09 %	GTP binding	protein biosynthesis
PBP1/YGR178C	722	0.168	4.3	2 (2)	9.09 %	mol. funct. unknown	mRNA polyadenylation

Table 40: Proteins which co–purify with PDS5/YMR076C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	17.2	3 (6)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	7.8	0 (3)	72.73 %	alcohol dehydrogenase	fermentation*
CDC19/YAL038W	500	0.893	6.0	2 (2)	50.00 %	pyruvate kinase	glycolysis*
CLU1/YMR012W	1277	0.227	2.6	2 (2)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	15.1	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	14.5	3 (3)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HOS3/YPL116W	697	0.157	7.0	3 (3)	22.73 %	histone deacetylase	histone deacetylation
ILV1/YER086W	576	0.312	7.5	2 (2)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
IMD1/YAR073W	403	0.287	10.4	0 (2)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD2/YHR216W	523	0.305	12.0	0 (3)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD3/YLR432W	523	0.464	12.0	↑	27.27 %	IMP dehydrogenase	GTP biosynthesis
MIS1/YBR084W	975	0.208	7.9	5 (6)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	19.1	6 (6)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	5.3	3 (3)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	3.0	2 (2)	31.82 %	6-phosphofructokinase	glycolysis
PSA1/YDL055C	361	0.6	10.2	2 (2)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL13A/YDL082W	199	0.652	11.1	0 (2)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	11.1	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL16B/YNL069C	198	0.723	12.6	2 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL18B/YNL301C	186	0.68	14.5	0 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	14.5	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	15.5	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL2A/YFR031C-A	254	0.773	4.3	0 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	4.3	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL30/YGL030W	105	0.865	27.6	2 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	33.6	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	33.6	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL8A/YHL033C	256	0.842	12.9	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL8B/YLL045C	256	0.849	12.9	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	7.9	0 (1)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	17.8	1 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	9.0	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS13/YDR064W	151	0.776	19.2	2 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	15.1	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	15.1	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	19.2	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	19.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS4B/YHR203C	261	0.709	10.7	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	10.7	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	13.5	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	13.5	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	8.1	4 (4)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	10.9	3 (3)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	18.2	2 (7)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	13.1	0 (5)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
SSB1/YDL229W	613	0.82	16.3	1 (7)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	14.2	0 (6)	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	4.1	2 (2)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	9.6	0 (2)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	13.9	0 (3)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	13.9	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	5.9	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	5.9	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	4.1	6 (6)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	5.7	0 (5)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	3.9	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	3.9	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	3.9	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	3.9	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YHR214C-B	NF	NF	3.8	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	13.0	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	13.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	13.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	3.9	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	6.2	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	6.2	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	6.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	7.1	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	7.1	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	7.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	7.1	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	8.9	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	6.1	0 (8)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	6.8	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	2.6	2 (2)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	7.1	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	4.0	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	3.0	0 (4)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.5	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	3.9	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

18 TAP–MuDPIT analysis of immune precipitations with PHO2–HPM (YDL106C) as the bait protein

Known interaction partners of PHO2 (YDL106C) according to MIPS (M), GRID (G) and YPD (Y) that were not recovered in this experiment: BAS1/YKR099W (Y, physical), CDC28/YBR160W (Y, physical), PHO4/YFR034C (M/Y, gen./phys.), SWI5/YDR146C (Y, physical);

Table 41: Potential interactors recovered through TAP–MuDPIT on PHO2/YDL106C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PHO2/YDL106C	559	0.148	33.1	22 (23)	4.55 %	transcr. factor	transcr.*
RPL35B/YDL136W	120	0.759	22.5	0 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL35A/YDL191W	120	0.798	22.5	↑	18.18 %	struct. const. of ribosome	protein biosynthesis
RPS5/YJR123W	225	0.838	21.3	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
YBL005W-A	NF	NF	6.4	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR170W-A	NF	NF	6.4	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261W-B	NF	NF	1.6	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-C	NF	NF	10.9	0 (2)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR026W	NF	NF	4.8	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YOL103W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML040W	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR256W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR028W	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR045C	NF	NF	2.7	0 (3)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YNL284C-B	NF	NF	1.6	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 42: Proteins which co–purify with PHO2/YDL106C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	9.1	3 (4)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	28.7	6 (7)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	7.5	2 (3)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	10.4	2 (2)	50.00 %	alcohol dehydrogenase	fermentation
CLU1/YMR012W	1277	0.227	9.1	7 (7)	45.45 %	mol. funct. unknown	translational initiation*
FBA1/YKL060C	359	0.869	24.0	5 (5)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
ILV1/YER086W	576	0.312	10.2	3 (3)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
KCS1/YDR017C	1050	0.144	3.9	3 (3)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	12.2	6 (7)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	9.7	2 (2)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	5.5	3 (3)	63.64 %	6-phosphofructokinase	glycolysis
RPL10/YLR075W	221	0.827	18.1	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL14B/YHL001W	138	0.68	21.7	0 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	21.7	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17B/YJL177W	184	0.68	15.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	184	0.809	15.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	10.1	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	10.1	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	30.2	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	26.4	0 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	26.4	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	7.5	3 (3)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	56.6	1 (7)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	48.7	0 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	22.3	3 (3)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	13.8	1 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	9.4	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL8A/YHL033C	256	0.842	16.0	0 (3)	50.00 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL8B/YLL045C	256	0.849	16.0	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	17.8	0 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	17.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	12.5	3 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS15/YOL040C	142	0.769	28.2	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS16B/YDL083C	143	0.764	18.9	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	18.9	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	16.4	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	16.4	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	56.9	0 (8)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	56.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	14.2	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS4B/YHR203C	261	0.709	11.9	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.9	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	12.2	4 (4)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	12.4	3 (3)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	5.9	0 (3)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	9.5	0 (4)	100.00 %	heat shock protein	protein folding*
TDH1/YJL052W	332	0.856	21.4	2 (5)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	19.0	0 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	56.3	7 (12)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	23.6	0 (9)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	23.6	↑	90.91 %	translation elongation factor	translational elongation
TRP5/YGL026C	707	0.32	4.0	2 (2)	22.73 %	tryptophan synthase	tryptophan biosynthesis
UGP1/YKL035W	499	0.33	10.6	3 (3)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	3.0	5 (5)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR010C	NF	NF	38.6	0 (11)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	38.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	38.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	38.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	38.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	3.4	0 (4)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YBR012W-A	NF	NF	27.5	0 (8)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	8.7	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	33.9	0 (9)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	33.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	33.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	9.6	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	29.3	0 (8)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	8.4	0 (9)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	11.8	0 (12)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	10.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	10.3	0 (11)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	10.3	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	4.9	2 (2)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	11.5	0 (13)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	10.8	0 (12)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	31.1	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	8.9	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	4.5	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	1.7	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR050C	NF	NF	1.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	1.8	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	2.3	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	2.3	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	3.0	0 (4)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	3.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	3.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

19 TAP–MuDPIT analysis of immune precipitations with PHO4–HPM (YFR034C) as the bait protein

Known interaction partners of PHO4 (YFR034C) according to MIPS (M), GRID (G) and YPD (Y) that were not recovered in this experiment: SNF5/YBR289W (Y, physical), GSP1/YLR293C (Y, physical), PHO80/YOL001W (M/Y, gen./phys.), TAF8/YML114C (Y, physical), MSN5/YDR335W (Y, physical), SUA7/YPR08 (M/Y, physical), PHO2/YDL106C (M/Y, gen./phys.), INO4/YOL108C (Y, physical), SNF6/YHL025W (Y, physical), SNF2/YOR290C (Y, physical), SWI1/YPL016 (Y, physical);

Table 43: Potential interactors recovered through TAP–MuDPIT on PHO4/YFR034C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PHO4/YFR034C	312	0.068	54.8	30 (30)	4.55 %	transcr. factor	phosphate metabolism*
ADE16/YLR028C	591	0.173	6.8	2 (2)	9.09 %	IMP cyclohydrolase*	aerobic respiration*
ADE3/YGR204W	946	0.277	3.6	1 (2)	9.09 %	formate-tetrahydrofolate ligase	purine base biosynthesis
APE3/YBR286W	563	0.332	7.1	2 (2)	4.55 %	aminopeptidase	vacuolar protein catabolism
ARO2/YGL148W	376	0.323	19.4	6 (6)	9.09 %	chorismate synthase	aromatic AA family biosynthesis
ARO4/YBR249C	370	0.527	13.2	2 (2)	13.64 %	deoxyphosphoheptonate aldolase	aromatic AA family biosynthesis
ASN1/YPR145W	572	0.368	12.2	2 (4)	9.09 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
BBC1/YJL020C	1157	0.135	5.4	4 (4)	4.55 %	myosin I binding	actin cytoskeleton organ. and biogen.
BCY1/YIL033C	416	0.178	15.6	5 (5)	9.09 %	cAMP-dep. protein kinase inhibitor	response to stress*
CCT4/YDL143W	528	0.225	9.3	2 (2)	9.09 %	chaperone	protein folding*
CCT8/YJL008C	568	0.203	3.9	2 (2)	9.09 %	chaperone	protein folding*
CDC33/YOL139C	213	0.387	24.4	4 (4)	13.64 %	translation initiation factor	translational initiation*
CDC73/YLR418C	393	0.136	8.1	2 (2)	4.55 %	Pol II transcr. elongation factor	RNA elongation from Pol II prom.
CHS5/YLR330W	671	0.152	10.7	3 (3)	13.64 %	mol. funct. unknown	conjug. with cell. fusion*
DBP2/YNL112W	546	0.422	10.6	3 (3)	4.55 %	RNA helicase	biological process unknown
DBP3/YGL078C	523	0.271	6.3	2 (2)	9.09 %	ATP dep. RNA helicase	35S prim. transcript processing*
DIG1/YPL049C	452	0.094	7.5	2 (2)	4.55 %	transcr. factor binding	invasive growth
EAP1/YKL204W	632	0.142	9.7	3 (3)	4.55 %	mol. funct. unknown	negative regulation of translation
EFT2/YDR385W	842	0.8	11.8	0 (5)	18.18 %	translation elongation factor	translational elongation
EFT1/YOR133W	842	0.804	11.8	↑	18.18 %	translation elongation factor	translational elongation
FAS1/YKL182W	2051	0.364	1.8	2 (2)	4.55 %	S–malonyltransferase*	fatty acid biosynthesis
FUN12/YAL035W	1002	0.355	6.4	3 (3)	4.55 %	translation initiation factor*	translational initiation

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
GLK1/YCL040W	500	0.158	7.2	2 (2)	9.09 %	glucokinase	carbohydrate metabolism
GLT1/YDL171C	2145	0.287	1.8	3 (3)	13.64 %	glutamate synthase (NADH)	glutamate biosynthesis
GLY1/YEL046C	387	0.33	13.7	3 (3)	18.18 %	threonine aldolase	threonine catabolism*
GUA1/YMR217W	525	0.462	22.9	7 (7)	9.09 %	GMP synthase (Glu hydrolyzing)	GMP metabolism
HEF3/YNL014W	1044	0.169	9.7	1 (7)	18.18 %	ATPase*	translational elongation
HOM3/YER052C	527	0.258	10.1	2 (2)	4.55 %	aspartate kinase	methionine metabolism*
HRB1/YNL004W	429	0.153	13.3	4 (4)	4.55 %	mol. funct. unknown	protein-nucleus import
HSP60/YLR259C	572	0.382	5.1	2 (2)	13.64 %	heat shock protein	protein folding*
IMD4/YML056C	524	0.471	25.6	2 (9)	9.09 %	IMP dehydrogenase	biological process unknown
KEM1/YGL173C	1528	0.194	2.0	2 (2)	13.64 %	recombinase*	35S prim. transcript processing*
KRI1/YNL308C	591	0.195	6.8	3 (3)	4.55 %	mol. funct. unknown	ribosome biogenesis
LYS21/YDL131W	440	0.329	7.7	0 (2)	4.55 %	homocitrate synthase	Lys biosynth., aminoadipic pathway
LYS20/YDL182W	428	0.321	7.9	↑	4.55 %	homocitrate synthase	Lys biosynth., aminoadipic pathway
MYO5/YMR109W	1219	0.185	2.5	2 (2)	4.55 %	microfilament motor	cell wall organ. and biogen.*
NFS1/YCL017C	497	0.226	24.3	6 (6)	18.18 %	cysteine desulfhydrase	iron ion homeostasis*
NMA1/YLR328W	401	0.209	13.7	3 (3)	4.55 %	nicotinamide–nucl. adenylyltransf.	NAD metabolism
NOP1/YDL014W	327	0.492	3.1	2 (2)	4.55 %	methyltransferase	rRNA modification*
NOP58/YOR310C	511	0.389	9.4	3 (3)	4.55 %	mol. funct. unknown	rRNA modification*
NSR1/YGR159C	414	0.493	20.0	5 (5)	9.09 %	RNA binding*	rRNA processing*
PAB1/YER165W	577	0.488	5.0	2 (2)	9.09 %	poly(A) binding	regulation of translational initiation
RPA135/YPR010C	1203	0.223	5.5	2 (2)	4.55 %	DNA-directed RNA polymerase	transcr. from Pol I prom.
RPA34/YJL148W	233	0.197	20.2	2 (2)	4.55 %	DNA-directed RNA polymerase	transcr. from Pol I prom.
RPL11B/YGR085C	174	0.727	20.1	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL11A/YPR102C	174	0.781	20.1	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL12B/YDR418W	165	0.766	37.0	0 (5)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL12A/YEL054C	165	0.605	37.0	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL16A/YIL133C	199	0.611	25.6	2 (4)	13.64 %	struct. const. of ribosome*	protein biosynthesis
RPL23A/YBL087C	137	0.624	27.7	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL23B/YER117W	137	0.648	27.7	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL24A/YGL031C	155	0.759	16.1	0 (4)	4.55 %	struct. const. of ribosome*	protein biosynthesis
RPL24B/YGR148C	155	0.756	16.1	↑	4.55 %	struct. const. of ribosome*	protein biosynthesis
RPL26B/YGR034W	129	0.677	40.3	0 (7)	9.09 %	struct. const. of ribosome*	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL26A/YLR344W	127	0.631	40.9	↑	9.09 %	struct. const. of ribosome*	protein biosynthesis
RPL29/YFR032C-A	59	0.682	45.8	3 (3)	4.55 %	struct. const. of ribosome	protein biosynthesis
RPL34A/YER056C-A	121	0.763	9.1	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL34B/YIL052C	121	0.781	9.1	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL35B/YDL136W	120	0.759	31.7	0 (3)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL35A/YDL191W	120	0.798	31.7	↑	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL36A/YMR194W	100	0.62	30.0	0 (3)	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL36B/YPL249C-A	100	0.8	30.0	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL38/YLR325C	78	0.775	38.5	3 (3)	4.55 %	struct. const. of ribosome	protein biosynthesis
RPL43B/YJR094W-A	92	0.571	29.3	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL43A/YPR043W	92	0.872	29.3	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL5/YPL131W	297	0.83	21.2	2 (2)	4.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL7A/YGL076C	244	0.76	20.1	1 (4)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL7B/YPL198W	244	0.716	16.4	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPP1A/YDL081C	106	0.714	20.8	2 (2)	4.55 %	struct. const. of ribosome	protein biosynthesis*
RPP2A/YOL039W	106	0.804	52.8	5 (5)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RPP2B/YDR382W	110	0.762	54.5	3 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS12/YOR369C	143	0.844	32.2	3 (3)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS19B/YNL302C	144	0.757	27.8	0 (4)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPS19A/YOL121C	144	0.794	27.8	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPS2/YGL123W	254	0.801	28.7	5 (5)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RPS23A/YGR118W	145	0.726	26.9	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS23B/YPR132W	145	0.789	26.9	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPS25A/YGR027C	108	0.716	23.1	0 (3)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS25B/YLR333C	108	0.612	23.1	↑	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS27B/YHR021C	82	0.66	28.0	0 (3)	4.55 %	struct. const. of ribosome	protein biosynthesis
RPS27A/YKL156W	82	0.361	28.0	↑	4.55 %	struct. const. of ribosome	protein biosynthesis
RPS29A/YLR388W	56	0.653	55.4	4 (5)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS29B/YDL061C	56	0.76	33.9	1 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPS5/YJR123W	225	0.838	12.9	3 (3)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPS7A/YOR096W	190	0.747	31.1	3 (4)	4.55 %	struct. const. of ribosome	protein biosynthesis
RPS7B/YNL096C	190	0.597	12.6	1 (2)	4.55 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS9A/YPL081W	197	0.507	28.4	1 (4)	4.55 %	struct. const. of ribosome	protein biosynthesis*
RPS9B/YBR189W	195	0.81	27.7	1 (4)	4.55 %	struct. const. of ribosome	protein biosynthesis*
RRB1/YMR131C	511	0.209	13.5	4 (4)	13.64 %	mol. funct. unknown	ribosome biogenesis
RRP5/YMR229C	1729	0.237	1.9	2 (2)	4.55 %	RNA binding*	rRNA processing*
RSP5/YER125W	809	0.186	6.2	2 (2)	4.55 %	ubiquitin-protein ligase	protein monoubiquitination*
SEC23/YPR181C	768	0.229	9.6	4 (4)	18.18 %	GTPase activator	ER to Golgi transport*
SES1/YDR023W	462	0.392	11.5	3 (3)	4.55 %	serine-tRNA ligase	AA activation
SHM2/YLR058C	469	0.589	11.9	3 (3)	13.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SIK1/YLR197W	504	0.37	18.3	5 (5)	4.55 %	mol. funct. unknown	rRNA modification*
SIN3/YOL004W	1536	0.15	3.0	2 (2)	4.55 %	histone deacetylase	regul. of Pol II prom. transcr.*
SNF1/YDR477W	633	0.188	10.7	3 (3)	18.18 %	SNF1A/AMP-activ. prot. kinase	prot. AA phosphoryl.*
SRM1/YGL097W	482	0.204	13.9	5 (5)	9.09 %	signal transducer	rRNA-nucleus export*
STE11/YLR362W	717	0.142	4.7	2 (2)	4.55 %	MAP kinase kinase kinase	prot. AA phosphoryl.*
STE50/YCL032W	346	0.12	12.1	2 (2)	4.55 %	protein kinase regulator	sig. transd. during conjug. with cell. fus.*
STM1/YLR150W	273	0.719	9.2	3 (3)	9.09 %	telomeric DNA binding	telomere maintenance*
TSR1/YDL060W	788	0.182	12.4	5 (5)	4.55 %	mol. funct. unknown	rRNA processing*
TUB1/YML085C	447	0.277	6.5	1 (2)	4.55 %	struct. const. of cytoskeleton	mitotic chromosome segregation*
TUB2/YFL037W	457	0.271	11.2	3 (3)	13.64 %	struct. const. of cytoskeleton	mitotic chromosome segregation*
TUB3/YML124C	445	0.241	8.1	1 (2)	4.55 %	struct. const. of cytoskeleton	mitotic chromosome segregation*
URA7/YBL039C	579	0.309	5.9	2 (2)	13.64 %	CTP synthase	phospholipid biosynthesis*
UTP7/YER082C	554	0.161	6.3	2 (2)	4.55 %	snoRNA binding	processing of 20S pre-rRNA
VIP1/YLR410W	1146	0.164	3.3	2 (2)	4.55 %	mol. funct. unknown	actin cytoskeleton organ. and biogen.
VPS1/YKR001C	704	0.249	15.2	8 (8)	9.09 %	GTPase	protein-vacuolar targeting*
VRP1/YLR337C	817	0.109	6.6	2 (2)	4.55 %	actin binding	actin filament organization*
YAR075W	157	0.329	15.9	0 (2)	4.55 %	mol. funct. unknown	biological process unknown
YBL101W-B	NF	NF	2.4	0 (4)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161W-B	NF	NF	2.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YFL002W-A	NF	NF	2.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210W-B	NF	NF	2.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR034C-D	NF	NF	2.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YCL019W	NF	NF	2.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261W-B	NF	NF	1.5	0 (3)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YGL068W	194	0.204	10.8	3 (3)	4.55 %	mol. funct. unknown	biological process unknown
YHR121W	187	0.168	17.1	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
YIL137C	946	0.173	2.4	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
YMR045C	NF	NF	2.6	0 (3)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR050C	NF	NF	1.7	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YMR237W	724	0.157	9.8	3 (3)	4.55 %	mol. funct. unknown	biological process unknown
YNL054W-B	NF	NF	1.5	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 44: Proteins which co–purify with PHO4/YFR034C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	16.0	8 (8)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	51.7	18 (23)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	14.1	2 (7)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	16.8	5 (6)	50.00 %	alcohol dehydrogenase	fermentation
ASN2/YGR124W	572	0.317	23.3	5 (7)	22.73 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
CDC19/YAL038W	500	0.893	38.4	15 (15)	50.00 %	pyruvate kinase	glycolysis*
CLU1/YMR012W	1277	0.227	7.0	5 (5)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	24.1	8 (8)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	40.9	19 (19)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HOS3/YPL116W	697	0.157	35.9	22 (22)	22.73 %	histone deacetylase	histone deacetylation
HYP2/YEL034W	157	0.814	23.6	3 (4)	27.27 %	translation initiation factor	translational initiation
ILV1/YER086W	576	0.312	13.2	4 (4)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
IMD1/YAR073W	403	0.287	23.1	0 (6)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD2/YHR216W	523	0.305	29.1	1 (10)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD3/YLR432W	523	0.464	44.2	5 (16)	27.27 %	IMP dehydrogenase	GTP biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
KAR2/YJL034W	682	0.44	4.4	0 (2)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
MIS1/YBR084W	975	0.208	20.0	12 (13)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	27.1	11 (11)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	35.6	24 (26)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	27.2	14 (16)	31.82 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	7.6	3 (3)	31.82 %	serine-type endopeptidase	sporulation*
PSA1/YDL055C	361	0.6	12.2	3 (3)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL10/YLR075W	221	0.827	45.7	9 (9)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL13A/YDL082W	199	0.652	29.1	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	30.7	1 (5)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL14B/YHL001W	138	0.68	26.8	0 (5)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	26.8	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL15A/YLR029C	204	0.783	28.9	2 (5)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	20.6	0 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL16B/YNL069C	198	0.723	25.8	2 (4)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17A/YKL180W	184	0.809	34.2	1 (5)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL17B/YJL177W	184	0.68	28.8	0 (4)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL18B/YNL301C	186	0.68	16.1	0 (3)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	16.1	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	40.7	0 (11)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	40.7	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL1B/YGL135W	217	0.832	27.6	0 (6)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	27.6	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	40.0	0 (8)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	41.4	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	30.6	3 (8)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	23.8	1 (6)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	40.8	6 (6)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	53.7	0 (9)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	53.7	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	39.6	6 (6)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	42.1	0 (14)	63.64 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL2B/YIL018W	254	0.764	42.1	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	28.9	11 (11)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL30/YGL030W	105	0.865	42.9	5 (5)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	73.5	2 (14)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	73.5	1 (13)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	23.8	4 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	47.0	1 (15)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	42.5	0 (14)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6A/YML073C	176	0.672	34.7	2 (6)	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL6B/YLR448W	176	0.627	34.1	2 (6)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	39.8	0 (11)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	45.3	1 (12)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	48.7	2 (10)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	46.1	2 (10)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	25.0	7 (7)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS11B/YBR048W	156	0.733	30.8	0 (5)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS11A/YDR025W	156	0.705	30.8	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS13/YDR064W	151	0.776	53.6	5 (5)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS14A/YCR031C	137	0.805	59.9	0 (9)	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS14B/YJL191W	138	0.59	59.4	↑	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS15/YOL040C	142	0.769	34.5	4 (4)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS16B/YDL083C	143	0.764	32.9	0 (5)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	32.9	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS17B/YDR447C	136	0.757	31.6	0 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS17A/YML024W	136	0.81	31.6	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS18A/YDR450W	146	0.775	48.6	0 (8)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	48.6	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	45.5	1 (11)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	45.5	1 (11)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	55.4	6 (6)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	60.0	0 (10)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	60.0	↑	90.91 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS24A/YER074W	135	0.816	55.6	0 (12)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS24B/YIL069C	135	0.756	55.6	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26B/YER131W	119	0.711	30.3	0 (4)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26A/YGL189C	119	0.781	30.3	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	47.9	10 (10)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS31/YLR167W	152	0.811	30.9	2 (3)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPS4B/YHR203C	261	0.709	40.2	0 (11)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	40.2	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	43.2	0 (10)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	43.2	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	42.5	0 (7)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	42.5	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	38.8	18 (18)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	47.2	15 (15)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	20.6	0 (10)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	27.5	2 (14)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	4.5	0 (3)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	10.1	0 (6)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	21.9	0 (11)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	21.9	↑	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	4.5	2 (2)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	53.0	6 (16)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	61.1	2 (25)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	87.0	20 (41)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	52.0	0 (27)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	52.0	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	9.8	7 (7)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
TRP5/YGL026C	707	0.32	19.4	8 (8)	22.73 %	tryptophan synthase	tryptophan biosynthesis
UBI4/YLL039C	381	0.317	4.2	0 (1)	22.73 %	protein tagging*	response to stress*
UGP1/YKL035W	499	0.33	42.3	14 (14)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	18.6	28 (28)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
VMA2/YBR127C	517	0.39	12.2	4 (4)	22.73 %	H^+–exporting ATPase	vacuolar acidification

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YAR009C	NF	NF	7.9	0 (8)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	30.0	0 (14)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	30.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	30.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	30.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	30.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	7.0	0 (11)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	13.8	0 (24)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	13.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	34.8	0 (15)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	34.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	34.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	34.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	14.7	0 (25)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	14.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	25.9	0 (13)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	13.7	0 (24)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	14.3	0 (23)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	14.1	0 (24)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	39.3	26 (32)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	14.7	0 (25)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	12.5	0 (22)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	32.0	0 (14)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	14.0	0 (24)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	7.3	0 (11)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	7.0	0 (11)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	5.8	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	4.7	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.7	0 (5)	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	5.6	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	5.1	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	5.6	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YML045W	NF	NF	5.6	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

20 TAP–MuDPIT analysis of immune precipitations with RTT102–HPM (YGR275W) as the bait protein

Known interaction partners of RTT102 (YGR275W) according to MIPS (M), GRID (G) and YPD (Y) that were not recovered in this experiment: VAN1/YML115C (M/G, physical), SUA7/YPR086W (M/G, physical);

Table 45: Potential interactors recovered through TAP–MuDPIT on RTT102/YGR275W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RTT102/YGR275W	186	0.108	75.8	37 (37)	9.09 %	mol. funct. unknown	biological process unknown
ARO4/YBR249C	370	0.527	9.2	2 (2)	13.64 %	deoxyphosphoheptonate aldolase	aromatic AA family biosynthesis
ARP7/YPR034W	477	0.112	75.3	73 (73)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
ARP9/YMR033W	467	0.158	70.4	77 (77)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
FYV6/YNL133C	173	0.11	22.0	3 (3)	4.55 %	mol. funct. unknown	DSB repair by nonhomol. end–joining
GSY2/YLR258W	705	0.165	4.3	2 (2)	4.55 %	glycogen (starch) synthase	glycogen metabolism
HSL1/YKL101W	1518	0.129	3.7	3 (3)	4.55 %	protein kinase	prot. AA phosphoryl.*
HTA2/YBL003C	132	0.544	34.8	0 (4)	4.55 %	DNA binding	chromatin assembly/disassembly
HTA1/YDR225W	132	0.654	34.8	↑	4.55 %	DNA binding	chromatin assembly/disassembly
HTL1/YCR020W-B	78	0.121	42.3	4 (4)	4.55 %	mol. funct. unknown	regulation of cell cycle*
LDB7/YBL006C	145	0.058	40.0	4 (4)	4.55 %	mol. funct. unknown	biological process unknown
NFI1/YOR156C	726	0.113	1.2	2 (2)	4.55 %	mol. funct. unknown	chromosome condensation
NFS1/YCL017C	497	0.226	9.1	2 (2)	18.18 %	cysteine desulfhydrase	iron ion homeostasis*
NPL6/YMR091C	435	0.142	57.5	19 (19)	4.55 %	mol. funct. unknown	protein-nucleus import
RIM1/YCR028C-A	135	0.308	22.2	2 (2)	4.55 %	single-stranded DNA binding	mitochondrial genome maintenance
RPL35B/YDL136W	120	0.759	34.2	0 (4)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL35A/YDL191W	120	0.798	34.2	↑	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL36A/YMR194W	100	0.62	23.0	0 (3)	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL36B/YPL249C-A	100	0.8	23.0	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL43B/YJR094W-A	92	0.571	34.8	0 (3)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL43A/YPR043W	92	0.872	34.8	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPS2/YGL123W	254	0.801	13.4	2 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RPS29B/YDL061C	56	0.76	33.9	1 (2)	18.18 %	struct. const. of ribosome	protein biosynthesis
RRB1/YMR131C	511	0.209	6.7	2 (2)	13.64 %	mol. funct. unknown	ribosome biogenesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RSC1/YGR056W	928	0.133	14.5	7 (8)	4.55 %	mol. funct. unknown	chromatin modeling
RSC2/YLR357W	889	0.146	39.9	26 (27)	4.55 %	mol. funct. unknown	chromatin modeling
RSC3/YDR303C	885	0.154	3.5	2 (2)	4.55 %	DNA binding	regulation of transcr., DNA-dep.*
RSC4/YKR008W	625	0.166	18.4	10 (10)	4.55 %	mol. funct. unknown	chromatin modeling
RSC58/YLR033W	502	0.142	63.5	23 (23)	4.55 %	mol. funct. unknown	chromatin modeling
RSC6/YCR052W	483	0.13	53.4	19 (19)	4.55 %	mol. funct. unknown	chromatin modeling
RSC8/YFR037C	557	0.128	54.6	35 (35)	4.55 %	mol. funct. unknown	chromatin modeling
RSC9/YML127W	581	0.129	31.3	15 (15)	4.55 %	chromatin binding	regul. of Pol II prom. transcr.*
SFH1/YLR321C	426	0.172	23.7	7 (7)	4.55 %	mol. funct. unknown	chromatin modeling
SNF12/YNR023W	566	0.124	33.4	13 (13)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SNF2/YOR290C	1703	0.155	24.7	25 (29)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SNF5/YBR289W	905	0.119	23.0	12 (12)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SNF6/YHL025W	332	0.083	22.3	5 (5)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
STH1/YIL126W	1359	0.186	38.3	36 (41)	9.09 %	ATPase*	meiosis*
SWI1/YPL016W	1314	0.152	9.6	8 (8)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SWI3/YJL176C	825	0.148	34.2	21 (21)	13.64 %	gen. pol II transcr. fact.	chromatin modeling
TAF14/YPL129W	244	0.144	21.3	4 (4)	9.09 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
YFL049W	623	0.143	17.2	8 (8)	9.09 %	mol. funct. unknown	biological process unknown
YHR097C	366	0.125	7.9	2 (2)	9.09 %	mol. funct. unknown	biological process unknown

Table 46: Proteins which co–purify with RTT102/YGR275W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CLU1/YMR012W	1277	0.227	3.5	2 (2)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	8.6	3 (3)	81.82 %	mol. funct. unknown	biological process unknown
KAR2/YJL034W	682	0.44	4.0	0 (2)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
KCS1/YDR017C	1050	0.144	12.1	8 (8)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	9.8	6 (7)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	20.0	5 (5)	95.45 %	mRNA binding	mRNA-nucleus export
PSA1/YDL055C	361	0.6	10.2	2 (2)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL10/YLR075W	221	0.827	36.2	5 (5)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL13A/YDL082W	199	0.652	16.1	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	16.1	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL15A/YLR029C	204	0.783	17.6	1 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	12.7	0 (2)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL16B/YNL069C	198	0.723	12.1	1 (2)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17A/YKL180W	184	0.809	12.5	1 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	24.9	0 (5)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	24.9	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL1B/YGL135W	217	0.832	15.7	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	15.7	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	15.0	0 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	15.5	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	16.2	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	23.1	1 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	23.9	3 (3)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	33.1	0 (4)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	33.1	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	30.2	5 (5)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	31.5	0 (8)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	31.5	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	9.6	4 (4)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL30/YGL030W	105	0.865	27.6	2 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	49.6	1 (7)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	49.6	1 (7)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	37.3	1 (9)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	32.9	0 (8)	68.18 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL6B/YLR448W	176	0.627	14.2	0 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL6A/YML073C	176	0.672	14.2	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	29.3	0 (5)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	29.3	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	34.0	1 (6)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	34.0	1 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS14A/YCR031C	137	0.805	7.3	0 (2)	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS14B/YJL191W	138	0.59	7.2	↑	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS16B/YDL083C	143	0.764	34.3	0 (4)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	34.3	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS17B/YDR447C	136	0.757	20.6	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS17A/YML024W	136	0.81	20.6	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS18A/YDR450W	146	0.775	26.7	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	26.7	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	7.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	12.9	1 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	23.8	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	23.8	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS24A/YER074W	135	0.816	24.4	0 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS24B/YIL069C	135	0.756	24.4	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26B/YER131W	119	0.711	22.7	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26A/YGL189C	119	0.781	22.7	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	25.8	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS6B/YBR181C	236	0.846	19.1	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	19.1	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	14.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	14.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	8.8	4 (4)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	11.4	3 (3)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	43.8	2 (21)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	41.5	1 (20)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	12.2	0 (5)	81.82 %	heat shock protein	response to stress*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA4/YER103W	642	0.184	9.0	0 (4)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	7.3	0 (3)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	7.3	↑	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	6.1	3 (3)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	9.6	0 (2)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	17.2	0 (4)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	19.3	1 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	14.6	0 (5)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	14.6	↑	90.91 %	translation elongation factor	translational elongation
UGP1/YKL035W	499	0.33	9.0	4 (4)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
YAR009C	NF	NF	2.3	0 (2)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	1.6	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	19.8	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	19.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	19.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	19.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	19.8	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	15.0	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	15.0	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	15.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	15.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	15.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	4.8	0 (5)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	4.8	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	5.4	0 (6)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	5.4	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	5.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	10.5	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	4.2	0 (5)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	7.2	0 (7)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	6.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	6.6	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YGR027W-B	NF	NF	6.0	0 (6)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	2.2	0 (2)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	2.8	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	2.8	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	2.8	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	2.8	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	2.2	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

21 TAP–MuDPIT analysis of immune precipitations with SDS22–HPM (YKL193C) as the bait protein

Table 47: Previously reported interaction partners of SDS22 (YKL193C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: CIC1/YHR052W (Y, physical), MHP1/YJL042W (Y, physical), PDC5/YLR134W (Y, physical), PMA1/YGL008C (G/Y, physical), SPB1/YCL054W (Y, physical), GSY1/YFR015C (Y, physical), FPR3/YML074C (Y, physical), YTM1/YOR272W (Y, physical), YGR130C (G/Y, physical), FIP1/YJR093C (Y, physical), SEN1/YLR430W (Y, physical), KEL1/YHR158C (Y, physical), NET1/YJL076W (G/Y, physical), NSR1/YGR159C (G/Y, physical), CLU1/YMR012W (Y, physical), ERB1/YMR049C (Y, physical), SUI2/YJR007W (Y, physical), NOP6/YDL213C (G/Y, physical), SGT1/YOR057W (Y, physical), GLC8/YMR311C (Y, physical), MDH1/YKL085W (Y, physical), SNF4/YGL115W (G/Y, physical), REG1/YDR028C (G/Y, physical), FIN1/YDR130C (Y, physical), FPR4/YLR449W (Y, physical), SCD5/YOR329C (Y, physical), RSE1/YML049C (G/Y, physical), NOP7/YGR103W (Y, physical), YOR227W (Y, physical), CFT1/YDR301W (Y, physical), GPH1/YPR160W (Y, physical), RVB1/YDR190C (G/Y, physical), YDR412W (Y, physical), ADH4/YGL256W (Y, physical), GSY2/YLR258W (Y, physical), SUI3/YPL237W (Y, physical), VHS3/YOR054C (Y, physical), PMA2/YPL036W (G/Y, physical), NSA1/YGL111W (Y, physical), KOG1/YHR186C (G/Y, physical), HXT6/YDR343C (G/Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SDS22/YKL193C	Bait	Bait	338	0.182	88.5	82 (82)	13.64 %	enzyme regulator*	chromosome segregation*
GLC7/YER133W	physical	G/Y	312	0.229	80.1	47 (50)	13.64 %	protein phosphatase type 1*	meiosis*
PPQ1/YPL179W	physical	G/Y	549	0.161	28.1	9 (10)	4.55 %	protein Ser/Thr phosphatase	protein AA dephosphorylation*
PPZ2/YDR436W	physical	G/Y	710	0.109	10.4	2 (12)	13.64 %	protein Ser/Thr phosphatase	sodium ion homeostasis
YPI1/YFR003C	physical	Y	155	0.121	54.8	18 (18)	13.64 %	mol. funct. unknown	biological process unknown

Table 48: Potential interactors recovered through TAP–MuDPIT on SDS22/YKL193C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
NIP100/YPL174C	868	0.122	4.1	2 (2)	4.55 %	protein binding*	mitotic anaphase B
PPZ1/YML016C	692	0.164	31.5	11 (21)	9.09 %	protein Ser/Thr phosphatase	sodium ion homeostasis

Continued from previous page ...

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SNF1/YDR477W	633	0.188	15.3	5 (5)	18.18 %	SNF1A/AMP-activ. prot. kinase	prot. AA phosphoryl.*
STU1/YBL034C	1513	0.148	2.0	2 (2)	4.55 %	struct. const. of cytoskeleton	microtubule nucleation
VPS8/YAL002W	1176	0.137	4.3	3 (3)	4.55 %	mol. funct. unknown	late endosome to vacuole transport
YBL010C	280	0.122	2.9	1 (1)	4.55 %	mol. funct. unknown	biological process unknown

Table 49: Proteins which co–purify with SDS22/YKL193C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	12.6	3 (4)	86.36 %	alcohol dehydrogenase	fermentation
PRB1/YEL060C	635	0.3	11.5	3 (3)	31.82 %	serine-type endopeptidase	sporulation*
RPL31A/YDL075W	113	0.737	23.9	0 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	23.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	13.6	1 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	21.5	2 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
SSA1/YAL005C	642	0.709	7.6	0 (4)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	7.7	↑	100.00 %	heat shock protein	protein folding*
TDH1/YJL052W	332	0.856	13.9	1 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	16.6	0 (4)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	38.6	2 (6)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	18.3	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	18.3	↑	90.91 %	translation elongation factor	translational elongation
UGP1/YKL035W	499	0.33	10.4	3 (3)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*

22 TAP–MuDPIT analysis of immune precipitations with SNF2–HPM (YOR290C) as the bait protein

Table 50: Previously reported interaction partners of SNF2 (YOR290C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: MRP49/YKL167C (Y, physical), YPL183C (Y, genetic), SRB4/YER022W (Y, physical), RPO26/YPR187W (Y, physical), UTP15/YMR093W (Y, physical), TFA2/YKR062W (Y, physical), PRP43/YGL120C (Y, physical), MRP20/YDR405W (Y, physical), CYR1/YJL005W (Y, physical), RPB10/YOR210W (Y, physical), STO1/YMR125W (Y, physical), MRPL23/YOR150W (Y, physical), IML1/YJR138W (Y, physical), UTP6/YDR449C (Y, physical), CHD1/YER164W (Y, physical), MED1/YPR070W (Y, physical), IMP3/YHR148W (Y, physical), IMG1/YCR046C (Y, physical), NRP1/YDL167C (Y, physical), UTP7/YER082C (Y, physical), RSC8/YFR037C (MIPS, physical), MRPL16/YBL038W (G/Y, physical), NAB6/YML117W (Y, physical), MRPL9/YGR220C (Y, physical), YGR054W (Y, genetic), RPB9/YGL070C (Y, physical), NUG1/YER006W (Y, physical), HRR25/YPL204W (Y, physical), HAP4/YKL109W (Y, physical), MRPL17/YNL252C (Y, physical), KIN28/YDL108W (Y, physical), RGR1/YLR071C (Y, physical), BUD3/YCL014W (Y, physical), TIF4632/YGL049C (Y, physical), DST1/YGL043W (Y, physical), PUB1/YNL016W (G/Y, physical), KRE33/YNL132W (Y, physical), RPB11/YOL005C (Y, physical), POL2/YNL262W (Y, physical), CCL1/YPR025C (Y, physical), RPB5/YBR154C (Y, physical), SIN4/YNL236W (M/G/Y, gen./phys.), VPS1/YKR001C (Y, genetic), HOS4/YIL112W (Y, physical), TAF5/YBR198C (Y, physical), UTP22/YGR090W (Y, physical), MRPL10/YNL284C (Y, physical), MRPL4/YLR439W (Y, physical), HCA4/YJL033W (Y, physical), EMG1/YLR186W (Y, physical), MRPL28/YDR462W (Y, physical), SPT7/YBR081C (M/G/Y, gen./phys.), HHF2/YNL030W (Y, physical), MED4/YOR174W (Y, physical), TFB3/YDR460W (Y, physical), GCN4/YEL009C (Y, physical), CPR1/YDR155C (G/Y, physical), SRB2/YHR041C (M/G/Y, gen./phys.), KRR1/YCL059C (Y, physical), SIF2/YBR103W (Y, physical), YDR115W (Y, genetic), RAD3/YER171W (Y, physical), RET2/YFR051C (Y, physical), MRPL6/YHR147C (Y, physical), DIM1/YPL266W (Y, physical), SSL1/YLR005W (Y, physical), BEM2/YER155C (Y, physical), KAP95/YLR347C (Y, physical), RPO21/YDL140C (Y, physical), NOB1/YOR056C (Y, physical), SEC27/YGL137W (Y, physical), RVB2/YPL235W (Y, physical), MRPL13/YKR006C (Y, physical), MED8/YBR193C (Y, physical), YML025C (Y, genetic), MRPL35/YDR322W (Y, physical), MPP10/YJR002W (Y, physical), SEC1/YDR164C (Y, physical), NRD1/YNL251C (Y, physical), MRPL36/YBR122C (Y, physical), ROX3/YBL093C (Y, physical), ENP1/YBR247C (Y, physical), UGT51/YLR189C (Y, physical), MHR1/YDR296W (Y, physical), TIF4631/YGR162W (Y, physical), HIR1/YBL008W (Y, physical), SET3/YKR029C (Y, physical), SOF1/YLL011W (Y, physical), SSN3/YPL042C (Y, physical), YGR081C (Y, genetic), SWI4/YER111C (Y, physical), SNT1/YCR033W (Y, physical), SNF11/YDR073W (M/G/Y, physical), PAN1/YIR006C (Y, physical), RPB3/YIL021W (Y, physical), IMG2/YCR071C (Y, physical), COP1/YDL145C (Y, physical), RPC10/YHR143W-A (Y, physical), MRPL1/YDR116C (Y, physical), RPB4/YJL140W (Y, physical), SRB7/YDR308C (Y, physical), MRPL25/YGR076C (Y, physical), MRPL20/YKR085C (Y, physical), LTV1/YKL143W (Y, physical), MRP7/YNL005C (Y, physical), ROM2/YLR371W (Y, physical), TSR1/YDL060W (Y, physical), TFG2/YGR005C (Y, physical), IMP4/YNL075W (Y, physical), MRPL8/YJL063C (Y, physical), MED2/YDL005C (Y, physical), MED6/YHR058C (Y, physical), MRPL51/YPR100W (Y, physical), TFA1/YKL028W (Y, physical), UTP20/YBL004W (Y, physical), CBF5/YLR175W (Y, physical), SUA7/YPR086W (Y, physical), SSN2/YDR443C (Y, physical), PET56/YOR201C (Y, physical), ECM16/YMR128W (Y, physical), RPB2/YOR151C (Y, physical), SRB6/YBR253W (Y, physical), MRPL27/YBR282W (Y, physical), SRB5/YGR104C (Y, physical), GAL11/YOL051W (M/G/Y, gen./phys.), MRPL24/YMR193W (Y, physical), SSL2/YIL143C (Y, physical), MRPL19/YNL185C (Y, physical), MRPL44/YMR225C (Y, physical), TFG1/YGR186W (Y, physical), NOP14/YDL148C (Y, physical), SPT20/YOL148C (M/G/Y, gen./phys.), TFB4/YPR056W (Y, physical), SYP1/YCR030C (Y, physical), MRPL7/YDR237W (Y, physical), HIR2/YOR038C (Y, physical), RPB7/YDR404C (Y, physical), NAM7/YMR080C (Y, physical), SRB8/YCR081W (Y, physical), SEC26/YDR238C (Y, physical), SGN1/YIR001C (Y, physical), NOC4/YPR144C (Y, physical), PGD1/YGL025C (Y, physical), MRPL3/YMR024W (Y, physical), RCL1/YOL010W (Y, physical), GCN5/YGR252W (M/G, genetic), TFB2/YPL122C (Y, physical), PHO4/YFR034C (Y, physical), LHP1/YDL051W (Y, physical), TFB1/YDR311W (Y, physical), HOS2/YGL194C (Y, physical), SAM1/YLR180W (Y, physical), SSN8/YNL025C (Y, physical), RIO2/YNL207W (G/Y, physical), NAB3/YPL190C (Y, physical), SMD3/YLR147C (Y, physical), RPB8/YOR224C (Y, physical), MED7/YOL135C (Y, physical), RRP12/YPL012W (Y, physical), MRH4/YGL064C (Y, physical), MRPL39/YML009C (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SNF2/YOR290C	Bait	Bait	1703	0.155	17.1	28 (30)	9.09 %	gen. pol II transcr. fact.	chromatin modeling

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Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	physical	Y	348	0.811	25.0	7 (9)	86.36 %	alcohol dehydrogenase	fermentation
ARP7/YPR034W	physical	Y	477	0.112	24.5	10 (10)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
ARP9/YMR033W	physical	Y	467	0.158	15.6	10 (10)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
NPL3/YDR432W	physical	Y	414	0.359	8.7	2 (2)	95.45 %	mRNA binding	mRNA-nucleus export
SNF12/YNR023W	physical	Y	566	0.124	27.9	13 (13)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SNF5/YBR289W	physical	G/Y	905	0.119	17.6	12 (12)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SNF6/YHL025W	physical	Y	332	0.083	19.6	5 (5)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SWI1/YPL016W	physical	Y	1314	0.152	18.2	18 (18)	9.09 %	gen. pol II transcr. fact.	chromatin modeling
SWI3/YJL176C	physical	M/G/Y	825	0.148	31.8	28 (28)	13.64 %	gen. pol II transcr. fact.	chromatin modeling
TAF14/YPL129W	physical	Y	244	0.144	16.0	4 (4)	9.09 %	gen. pol II transcr. fact.	transcr. init. from Pol II prom.*
YFL049W	physical	Y	623	0.143	27.1	12 (12)	9.09 %	mol. funct. unknown	biological process unknown

Table 51: Potential interactors recovered through TAP–MuDPIT on SNF2/YOR290C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CHS5/YLR330W	671	0.152	4.0	2 (2)	13.64 %	mol. funct. unknown	conjug. with cell. fusion*
PAB1/YER165W	577	0.488	11.8	4 (4)	9.09 %	poly(A) binding	regulation of translational initiation
RPL11B/YGR085C	174	0.727	14.4	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL11A/YPR102C	174	0.781	14.4	↑	9.09 %	struct. const. of ribosome	protein biosynthesis*
RPL16A/YIL133C	199	0.611	13.6	2 (2)	13.64 %	struct. const. of ribosome*	protein biosynthesis
RPL26A/YLR344W	127	0.631	14.2	0 (2)	9.09 %	struct. const. of ribosome*	protein biosynthesis
RPL26B/YGR034W	129	0.677	21.7	1 (3)	9.09 %	struct. const. of ribosome*	protein biosynthesis
RPL34A/YER056C-A	121	0.763	6.6	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL34B/YIL052C	121	0.781	6.6	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
RPL35B/YDL136W	120	0.759	30.8	0 (3)	18.18 %	struct. const. of ribosome	protein biosynthesis
RPL35A/YDL191W	120	0.798	30.8	↑	18.18 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL36A/YMR194W	100	0.62	23.0	0 (3)	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPL36B/YPL249C-A	100	0.8	23.0	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis
RPS12/YOR369C	143	0.844	18.9	2 (2)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS2/YGL123W	254	0.801	17.3	3 (3)	18.18 %	struct. const. of ribosome	protein biosynthesis*
RTT102/YGR275W	186	0.108	51.1	7 (7)	9.09 %	mol. funct. unknown	biological process unknown
STH1/YIL126W	1359	0.186	2.4	1 (3)	9.09 %	ATPase*	meiosis*
STM1/YLR150W	273	0.719	12.1	2 (2)	9.09 %	telomeric DNA binding	telomere maintenance*
YDL053C	185	0.127	20.0	2 (2)	4.55 %	mol. funct. unknown	biological process unknown
YGR161C-C	NF	NF	4.5	0 (2)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 52: Proteins which co–purify with SNF2/YOR290C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH2/YMR303C	348	0.505	8.9	1 (3)	72.73 %	alcohol dehydrogenase	fermentation*
CDC19/YAL038W	500	0.893	10.6	4 (4)	50.00 %	pyruvate kinase	glycolysis*
CTS2/YDR371W	511	0.137	12.1	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
HOS3/YPL116W	697	0.157	11.5	5 (5)	22.73 %	histone deacetylase	histone deacetylation
HSC82/YMR186W	705	0.581	4.4	1 (2)	31.82 %	chaperone*	response to stress*
IMD1/YAR073W	403	0.287	14.9	0 (3)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD2/YHR216W	523	0.305	15.5	0 (4)	22.73 %	IMP dehydrogenase	GTP biosynthesis
IMD3/YLR432W	523	0.464	18.0	1 (5)	27.27 %	IMP dehydrogenase	GTP biosynthesis
MIS1/YBR084W	975	0.208	4.9	3 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
PFK1/YGR240C	987	0.466	9.6	7 (8)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	11.5	6 (7)	31.82 %	6-phosphofructokinase	glycolysis
PSA1/YDL055C	361	0.6	8.0	2 (2)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL13A/YDL082W	199	0.652	20.6	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL13B/YMR142C	199	0.742	20.6	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL14B/YHL001W	138	0.68	20.3	0 (4)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL14A/YKL006W	138	0.684	20.3	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL15A/YLR029C	204	0.783	23.0	1 (4)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	18.1	0 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL16B/YNL069C	198	0.723	14.1	3 (3)	27.27 %	struct. const. of ribosome*	protein biosynthesis
RPL17A/YKL180W	184	0.809	34.2	1 (5)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL17B/YJL177W	184	0.68	34.2	1 (5)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL18B/YNL301C	186	0.68	16.1	0 (3)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	16.1	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	24.3	0 (6)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	24.3	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	20.6	0 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	21.3	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	28.8	1 (6)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	21.9	0 (5)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	31.0	4 (4)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	18.4	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	18.4	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	26.8	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	15.7	0 (5)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	15.7	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	14.2	5 (5)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL30/YGL030W	105	0.865	39.0	3 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	35.4	1 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	35.4	1 (4)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	16.2	4 (4)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	16.9	1 (5)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	16.9	1 (5)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6B/YLR448W	176	0.627	10.8	1 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	12.1	0 (4)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	12.1	↑	50.00 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL9A/YGL147C	191	0.771	25.1	1 (5)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	25.1	1 (5)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	8.7	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS11B/YBR048W	156	0.733	17.3	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS11A/YDR025W	156	0.705	17.3	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS14A/YCR031C	137	0.805	22.6	0 (2)	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS14B/YJL191W	138	0.59	22.5	↑	22.73 %	struct. const. of ribosome*	protein biosynthesis*
RPS15/YOL040C	142	0.769	16.9	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS16B/YDL083C	143	0.764	27.3	0 (3)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS16A/YMR143W	143	0.677	27.3	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS17B/YDR447C	136	0.757	20.6	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS17A/YML024W	136	0.81	20.6	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS18A/YDR450W	146	0.775	24.0	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	24.0	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	18.4	1 (4)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	18.4	1 (4)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	24.6	0 (3)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	24.6	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS24A/YER074W	135	0.816	25.2	0 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS24B/YIL069C	135	0.756	25.2	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26B/YER131W	119	0.711	20.2	0 (3)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26A/YGL189C	119	0.781	20.2	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS4B/YHR203C	261	0.709	12.6	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	12.6	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	14.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	14.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	6.7	3 (3)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	10.3	3 (3)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	4.2	0 (2)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	4.2	↑	100.00 %	heat shock protein	protein folding*
SSB1/YDL229W	613	0.82	9.6	0 (4)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	9.6	↑	59.09 %	chaperone*	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
TDH1/YJL052W	332	0.856	26.2	2 (6)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	30.4	0 (10)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	30.4	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	14.4	0 (5)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	14.4	↑	90.91 %	translation elongation factor	translational elongation
URA2/YJL130C	2214	0.286	2.6	4 (4)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
VMA2/YBR127C	517	0.39	5.8	2 (2)	22.73 %	H^+–exporting ATPase	vacuolar acidification
YAR009C	NF	NF	4.7	0 (4)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	3.2	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	4.8	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	3.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	13.9	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	13.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	13.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	13.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	13.9	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	3.9	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	9.1	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	9.1	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	9.1	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	9.1	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	5.5	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	5.5	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	4.5	0 (2)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	4.3	0 (6)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	7.3	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	6.7	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	3.6	2 (3)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	6.7	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	6.0	0 (8)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YGR038C-A	NF	NF	6.4	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	4.8	0 (7)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	4.3	0 (6)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	4.4	0 (5)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	4.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	4.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	4.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	4.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

23 TAP–MuDPIT analysis of immune precipitations with SPO12–HPM (YHR152W) as the bait protein

Table 53: Previously reported interaction partners of SPO12 (YHR152W) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: YLR016C (M/G/Y, physical), MCM21/YDR318W (M/G/Y, physical), SRB4/YER022W (M/G/Y, physical), YPR152C (M/G/Y, physical), YLR132C (M/G/Y, physical), DBF2/YGR092W (M/G/Y, genetic), FIR1/YER032W (M/G/Y, physical), MEC3/YLR288C (M/G/Y, physical), BAT2/YJR148W (M/G/Y, physical), CDC15/YAR019C (MIPS, genetic), CLA4/YNL298W (Y, genetic), DCS2/YOR173W (M/G/Y, physical), CDH1/YGL003C (M/G/Y, genetic), SUM1/YDR310C (G/Y, physical), SRV2/YNL138W (G/Y, physical), CSM1/YCR086W (M/G/Y, physical), SET2/YJL168C (M/G/Y, physical), YDR267C (M/G/Y, physical), YPR118W (M/G/Y, physical), LTE1/YAL024C (MIPS, genetic), FUR1/YHR128W (M/G/Y, physical), OSH3/YHR073W (M/G/Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SPO12/YHR152W	Bait	Bait	173	0.118	41.6	12 (12)	4.55 %	mol. funct. unknown	regul. of exit from mitosis*
PSE1/YMR308C	physical	G/Y	1089	0.18	3.5	2 (2)	4.55 %	protein carrier	mRNA-nucleus export

Table 54: Potential interactors recovered through TAP–MuDPIT on SPO12/YHR152W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACT1/YFL039C	375	0.711	16.3	4 (4)	18.18 %	struct. const. of cytoskeleton	cell wall organ. and biogen.*
ADO1/YJR105W	340	0.37	9.1	2 (2)	4.55 %	adenosine kinase	purine base metabolism
AHP1/YLR109W	176	0.549	21.0	2 (2)	9.09 %	thioredoxin peroxidase	regulation of redox homeostasis*
ALD6/YPL061W	500	0.52	8.8	3 (3)	4.55 %	aldehyde dehydrogenase	acetate biosynthesis
AZR1/YGR224W	613	0.138	2.0	2 (2)	9.09 %	transporter	transport
BMH1/YER177W	267	0.323	8.2	1 (2)	18.18 %	DNA binding	pseudohyphal growth*
CPR1/YDR155C	162	0.614	34.0	3 (4)	4.55 %	peptidyl-prolyl cis-trans isomerase	protein metabolism
CYS3/YAL012W	394	0.42	7.4	2 (2)	4.55 %	cystathionine-gamma-lyase	sulfur AA metabolism*
EFT2/YDR385W	842	0.8	10.7	0 (7)	18.18 %	translation elongation factor	translational elongation

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
EFT1/YOR133W	842	0.804	10.7	↑	18.18 %	translation elongation factor	translational elongation
ENO1/YGR254W	437	0.871	29.3	4 (10)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
ENO2/YHR174W	437	0.892	44.4	10 (16)	18.18 %	phosphopyruvate hydratase	gluconeogenesis*
GPM1/YKL152C	247	0.811	9.3	2 (2)	9.09 %	phosphoglycerate mutase	gluconeogenesis*
HSP12/YFL014W	109	0.639	24.8	2 (2)	4.55 %	heat shock protein	response to oxidative stress*
HSP42/YDR171W	375	0.182	6.1	2 (2)	9.09 %	chaperone*	response to stress*
HXK2/YGL253W	486	0.643	6.2	2 (2)	4.55 %	hexokinase	fructose metabolism
PDC1/YLR044C	563	0.904	27.5	9 (10)	18.18 %	pyruvate decarboxylase	pyruvate metabolism*
PGI1/YBR196C	554	0.681	5.2	2 (2)	4.55 %	glucose-6–P_i isomerase	gluconeogenesis*
PGK1/YCR012W	416	0.815	51.9	18 (18)	18.18 %	phosphoglycerate kinase	gluconeogenesis*
RHR2/YIL053W	271	0.604	10.7	1 (2)	4.55 %	glycerol-1-phosphatase	response to osmotic stress*
RPS12/YOR369C	143	0.844	11.9	2 (2)	13.64 %	struct. const. of ribosome	protein biosynthesis
RPS19B/YNL302C	144	0.757	18.1	0 (2)	9.09 %	struct. const. of ribosome	protein biosynthesis
RPS19A/YOL121C	144	0.794	18.1	↑	9.09 %	struct. const. of ribosome	protein biosynthesis
TIF2/YJL138C	395	0.751	16.2	0 (4)	4.55 %	translation initiation factor*	translational initiation*
TIF1/YKR059W	395	0.753	16.2	↑	4.55 %	translation initiation factor	translational initiation
TRP3/YKL211C	484	0.184	7.6	2 (2)	13.64 %	anthranilate synthase*	tryptophan biosynthesis
TRX2/YGR209C	104	0.425	26.0	2 (2)	9.09 %	thiol-disulfide exchange intermediate	response to oxidative stress*
YHB1/YGR234W	399	0.267	16.0	4 (4)	18.18 %	mol. funct. unknown	response to stress
YNL134C	376	0.239	8.0	2 (2)	4.55 %	alcohol dehydrogenase (NADP+)	biological process unknown
YPL257W-B	NF	NF	1.8	0 (2)	4.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 55: Proteins which co–purify with SPO12/YHR152W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	26.7	7 (9)	86.36 %	alcohol dehydrogenase	fermentation

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH2/YMR303C	348	0.505	9.5	1 (3)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	6.4	1 (2)	50.00 %	alcohol dehydrogenase	fermentation
ASN2/YGR124W	572	0.317	4.7	1 (2)	22.73 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
CDC19/YAL038W	500	0.893	28.8	10 (11)	50.00 %	pyruvate kinase	glycolysis*
CLU1/YMR012W	1277	0.227	2.8	2 (2)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	21.5	8 (8)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	26.5	6 (6)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HSC82/YMR186W	705	0.581	14.9	2 (8)	31.82 %	chaperone*	response to stress*
HSP82/YPL240C	709	0.518	11.1	0 (6)	27.27 %	chaperonin ATPase	response to stress*
ILV1/YER086W	576	0.312	10.8	3 (3)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
KAR2/YJL034W	682	0.44	1.8	0 (1)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
KCS1/YDR017C	1050	0.144	21.5	19 (19)	31.82 %	inositol/phosphatidylinositol kin.	response to stress*
MIS1/YBR084W	975	0.208	5.6	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	23.9	7 (7)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	6.9	4 (4)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	2.8	2 (2)	31.82 %	6-phosphofructokinase	glycolysis
PSA1/YDL055C	361	0.6	10.2	3 (3)	45.45 %	mannose-1–P_i guanylyltransferase	protein AA glycosylation*
RPL13A/YDL082W	199	0.652	16.1	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL13B/YMR142C	199	0.742	16.1	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL17B/YJL177W	184	0.68	15.8	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPL17A/YKL180W	184	0.809	15.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	13.2	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	13.2	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	27.8	0 (4)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	28.7	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	10.6	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	10.6	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	24.6	3 (3)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL28/YGL103W	149	0.705	26.8	4 (4)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	11.8	0 (3)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	11.8	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	7.2	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPL31A/YDL075W	113	0.737	32.7	1 (3)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	24.8	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	22.3	3 (3)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	23.2	1 (5)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	18.8	0 (4)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL6B/YLR448W	176	0.627	13.1	0 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL6A/YML073C	176	0.672	13.1	↑	27.27 %	struct. const. of ribosome*	protein biosynthesis*
RPL8A/YHL033C	256	0.842	12.1	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL8B/YLL045C	256	0.849	12.1	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	28.3	0 (5)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	38.2	1 (6)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	7.7	2 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS11B/YBR048W	156	0.733	17.9	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS11A/YDR025W	156	0.705	17.9	↑	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPS15/YOL040C	142	0.769	30.3	3 (3)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	27.4	0 (5)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	27.4	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	7.5	0 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	7.5	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	21.5	2 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	19.2	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	19.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	16.7	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*
RPS31/YLR167W	152	0.811	13.2	1 (2)	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPS4B/YHR203C	261	0.709	15.3	0 (3)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	15.3	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS6B/YBR181C	236	0.846	20.3	0 (4)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS6A/YPL090C	236	0.837	20.3	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPS8A/YBL072C	200	0.747	15.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPS8B/YER102W	200	0.718	15.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
SHM1/YBR263W	565	0.264	9.2	4 (4)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	29.2	10 (10)	95.45 %	RNA binding	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
SSA1/YAL005C	642	0.709	43.8	6 (23)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	43.8	4 (21)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	10.5	0 (5)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	7.3	0 (4)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	25.3	1 (12)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	23.2	0 (11)	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	4.1	2 (2)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	29.5	4 (6)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	30.1	1 (7)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	28.0	1 (7)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	22.7	0 (7)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	22.7	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	5.1	3 (3)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
UGP1/YKL035W	499	0.33	14.2	4 (4)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	4.0	6 (6)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
VMA2/YBR127C	517	0.39	8.5	3 (3)	22.73 %	H^+–exporting ATPase	vacuolar acidification
YAR009C	NF	NF	6.5	0 (5)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	4.4	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	4.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	7.0	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	7.0	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	4.9	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	5.3	0 (7)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	8.0	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YDR210C-D	NF	NF	7.4	0 (9)	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	7.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	7.0	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	8.0	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	4.6	3 (4)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	6.9	0 (9)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	5.3	0 (7)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	5.3	0 (7)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	4.3	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	7.4	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	3.5	0 (4)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	3.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	5.1	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	5.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	5.4	0 (4)	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	6.3	0 (7)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	5.1	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

24 TAP–MuDPIT analysis of immune precipitations with YAK1–HPM (YJL141C) as the bait protein

Table 56: Previously reported interaction partners of YAK1 (YJL141C) according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: CIC1/YHR052W (Y, physical), LOC1/YFR001W (Y, physical), BMS1/YPL217C (Y, physical), SPB1/YCL054W (Y, physical), CDC46/YLR274W (Y, physical), VPS1/YKR001C (G/Y, physical), FPR3/YML074C (Y, physical), ENP1/YBR247C (Y, physical), AHP1/YLR109W (G/Y, physical), MCA1/YOR197W (M/G/Y, physical), NIP7/YPL211W (Y, physical), SEH1/YGL100W (Y, physical), NOP1/YDL014W (Y, physical), CDC39/YCR093W (G/Y, physical), IMD3/YLR432W (Y, physical), YER077C (Y, physical), PET127/YOR017W (Y, physical), TIS11/YLR136C (Y, physical), KRI1/YNL308C (Y, physical), DNM1/YLL001W (G/Y, physical), CKS1/YBR135W (Y, physical), DED81/YHR019C (Y, physical), RRP12/YPL012W (Y, physical), MSS116/YDR194C (Y, physical), EBP2/YKL172W (Y, physical), TSA2/YDR453C (G/Y, physical), COF1/YLL050C (Y, physical), DCS1/YLR270W (G/Y, physical), PUF6/YDR496C (Y, physical), LSP1/YPL004C (Y, physical), KRE33/YNL132W (Y, physical), ERB1/YMR049C (Y, physical), CTF4/YPR135W (Y, physical), TIF6/YPR016C (Y, physical), IMD4/YML056C (Y, physical), PWP1/YLR196W (Y, physical), SLT2/YHR030C (Y, physical), YRA1/YDR381W (Y, physical), YLR241W (G/Y, physical), UTP22/YGR090W (Y, physical), SSF1/YHR066W (Y, physical), YTM1/YOR272W (Y, physical), LST4/YKL176C (Y, physical), NMD3/YHR170W (Y, physical), PIL1/YGR086C (Y, physical), POP2/YNR052C (Y, physical), NOP12/YOL041C (Y, physical), YBL104C (Y, physical), MCM3/YEL032W (Y, physical), MCM2/YBL023C (Y, physical), GDB1/YPR184W (G/Y, physical), DBP10/YDL031W (Y, physical), UBR1/YGR184C (G/Y, physical), DCS2/YOR173W (G/Y, physical), RAD50/YNL250W (G/Y, physical), SSZ1/YHR064C (Y, physical), ELA1/YNL230C (G/Y, physical), CDC53/YDL132W (Y, physical), GTS1/YGL181W (GRID, physical), HRT1/YOL133W (M/G/Y, physical), HAT1/YPL001W (Y, physical), ECM10/YEL030W (Y, physical), ILS1/YBL076C (Y, physical), UBP15/YMR304W (G/Y, physical), NOP7/YGR103W (Y, physical), YKL014C (Y, physical), DIA2/YOR080W (G/Y, physical), RPF2/YKR081C (Y, physical), SKP1/YDR328C (Y, physical), SSF2/YDR312W (Y, physical), UTP10/YJL109C (Y, physical), NOG1/YPL093W (Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YAK1/YJL141C	Bait	Bait	807	0.125	75.0	110 (110)	4.55 %	protein kinase	prot. AA phosphoryl.*
BMH1/YER177W	physical	Y	267	0.323	9.0	1 (2)	18.18 %	DNA binding	pseudohyphal growth*
BMH2/YDR099W	physical	Y	273	0.385	8.8	1 (2)	9.09 %	DNA binding	pseudohyphal growth*
YPL247C	physical	G/Y	523	0.099	89.5	81 (81)	4.55 %	mol. funct. unknown	biological process unknown

Table 57: Potential interactors recovered through TAP–MuDPIT on YAK1/YJL141C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CAF20/YOR276W	161	0.356	17.4	2 (2)	18.18 %	translation regulator	negative regulation of translation
GLT1/YDL171C	2145	0.287	1.4	2 (2)	13.64 %	glutamate synthase (NADH)	glutamate biosynthesis
GLY1/YEL046C	387	0.33	8.3	2 (2)	18.18 %	threonine aldolase	threonine catabolism*
HEF3/YNL014W	1044	0.169	7.7	0 (6)	18.18 %	ATPase*	translational elongation
KEM1/YGL173C	1528	0.194	1.8	2 (2)	13.64 %	recombinase*	35S prim. transcript processing*
NFS1/YCL017C	497	0.226	5.8	2 (2)	18.18 %	cysteine desulfhydrase	iron ion homeostasis*
RIB4/YOL143C	169	0.211	20.1	2 (2)	13.64 %	6,7-dimethyl-8-ribityllumazine synthase	vitamin B2 biosynthesis
YJL206C	758	0.146	3.7	2 (2)	4.55 %	mol. funct. unknown	biological process unknown

Table 58: Proteins which co–purify with YAK1/YJL141C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ACS2/YLR153C	683	0.371	19.3	8 (9)	40.91 %	acetate-CoA ligase	acetyl-CoA biosynthesis
ADH1/YOL086C	348	0.811	64.1	16 (22)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	30.5	5 (11)	72.73 %	alcohol dehydrogenase	fermentation*
ADH3/YMR083W	375	0.3	18.4	3 (5)	50.00 %	alcohol dehydrogenase	fermentation
ASN2/YGR124W	572	0.317	3.7	1 (2)	22.73 %	Asp synthase (Glu–hydrol.)	asparagine biosynthesis
CDC19/YAL038W	500	0.893	6.0	2 (2)	50.00 %	pyruvate kinase	glycolysis*
CTS2/YDR371W	511	0.137	19.8	6 (6)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	39.0	8 (8)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HYP2/YEL034W	157	0.814	47.1	5 (6)	27.27 %	translation initiation factor	translational initiation
KAR2/YJL034W	682	0.44	3.4	0 (2)	36.36 %	chaperone*	karyogamy during conjug. with cell. fus.*
MIS1/YBR084W	975	0.208	5.1	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
NPL3/YDR432W	414	0.359	19.1	7 (7)	95.45 %	mRNA binding	mRNA-nucleus export
PFK1/YGR240C	987	0.466	9.4	6 (6)	63.64 %	6-phosphofructokinase	glycolysis
RPL31A/YDL075W	113	0.737	22.1	1 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	14.2	0 (1)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	10.2	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	10.2	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	37.7	1 (7)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	37.7	1 (7)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	25.4	0 (3)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	25.4	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS4B/YHR203C	261	0.709	11.1	0 (2)	59.09 %	struct. const. of ribosome	protein biosynthesis
RPS4A/YJR145C	261	0.695	11.1	↑	59.09 %	struct. const. of ribosome	protein biosynthesis
SRO9/YCL037C	466	0.264	25.1	7 (7)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	13.2	1 (6)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	11.3	0 (5)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
TDH1/YJL052W	332	0.856	32.8	3 (13)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	38.6	1 (14)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	55.1	12 (24)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	35.2	0 (14)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	35.2	↑	90.91 %	translation elongation factor	translational elongation
TFP1/YDL185W	1071	0.305	3.2	2 (2)	36.36 %	H^+–exporting ATPase*	vacuolar acidification*
TRP5/YGL026C	707	0.32	6.4	3 (3)	22.73 %	tryptophan synthase	tryptophan biosynthesis
UGP1/YKL035W	499	0.33	14.2	6 (6)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	1.8	2 (2)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	3.1	0 (3)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	2.1	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	3.2	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YJR027W	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	2.1	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	2.1	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	13.4	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	13.4	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-C	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	5.5	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	5.5	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	5.5	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	6.0	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	5.5	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	5.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	22.6	10 (16)	54.55 %	translation elongation factor	translational elongation

25 TAP–MuDPIT analysis of immune precipitations with YHR115C–HPM as the bait protein

Table 59: Previously reported interaction partners of YHR115C according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: RVB1/YDR190C (Y, physical), RPT4/YOR259C (Y, physical), YBR042C (M/G/Y, physical), RPT2/YDL007W (Y, physical), YEL041W (M/G/Y, physical), ERG1/YGR175C (Y, physical), GYP8/YFL027C (M/G/Y, physical), STI1/YOR027W (Y, physical), YOR215C (M/G/Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YHR115C	Bait	Bait	416	0.151	34.4	18 (19)	9.09 %	mol. funct. unknown	biological process unknown
CDC123/YLR215C	physical	M/G/Y	360	0.142	11.7	3 (3)	4.55 %	mol. funct. unknown	biological process unknown
RPL40A/YIL148W	physical	Y	128	0.742	11.7	0 (3)	18.18 %	struct. const. of ribosome*	protein biosynthesis*
RPS31/YLR167W	physical	Y	152	0.811	9.9	↑	31.82 %	struct. const. of ribosome*	protein biosynthesis*
UBI4/YLL039C	physical	Y	381	0.317	3.9	↑	22.73 %	protein tagging*	response to stress*
RPL40B/YKR094C	physical	Y	128	0.742	11.7	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis*
SKP1/YDR328C	physical	Y	194	0.193	16.0	2 (2)	9.09 %	ubiquitin-protein ligase	ubiquitin–dep. prot. catabol.*
YNL116W	physical	G/Y	522	0.13	43.1	21 (22)	9.09 %	mol. funct. unknown	biological process unknown
YNL311C	physical	G/Y	763	0.141	17.6	15 (15)	9.09 %	protein binding	ubiquitin–dep. prot. catabol.

Table 60: Potential interactors recovered through TAP–MuDPIT on YHR115C–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
DBP3/YGL078C	523	0.271	5.4	2 (2)	9.09 %	ATP dep. RNA helicase	35S prim. transcript processing*
GCD11/YER025W	527	0.333	11.0	4 (4)	4.55 %	translation initiation factor	translational initiation
JIP5/YPR169W	514	0.166	4.5	2 (2)	9.09 %	mol. funct. unknown	biological process unknown
MKT1/YNL085W	830	0.203	3.9	2 (2)	9.09 %	mol. funct. unknown	viral life cycle
SEC16/YPL085W	2195	0.141	1.0	2 (2)	4.55 %	struct. molecule	vesicle-mediated transport*

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YBL101W-B	NF	NF	1.4	0 (2)	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR410W-B	NF	NF	1.4	↑	4.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161W-B	NF	NF	1.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YFL002W-A	NF	NF	1.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210W-B	NF	NF	1.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR034C-D	NF	NF	1.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YCL019W	NF	NF	1.4	↑	13.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR026W	NF	NF	4.8	0 (2)	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YOL103W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML040W	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR256W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-A	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR028W	NF	NF	4.8	↑	9.09 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

Table 61: Proteins which co–purify with YHR115C–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
ADH1/YOL086C	348	0.811	21.6	6 (8)	86.36 %	alcohol dehydrogenase	fermentation
ADH2/YMR303C	348	0.505	5.5	0 (2)	72.73 %	alcohol dehydrogenase	fermentation*
CLU1/YMR012W	1277	0.227	7.4	6 (6)	45.45 %	mol. funct. unknown	translational initiation*
CTS2/YDR371W	511	0.137	19.2	9 (9)	81.82 %	mol. funct. unknown	biological process unknown
FBA1/YKL060C	359	0.869	10.3	2 (2)	63.64 %	fructose-bisphosphate aldolase	gluconeogenesis*
HYP2/YEL034W	157	0.814	22.9	2 (2)	27.27 %	translation initiation factor	translational initiation
MIS1/YBR084W	975	0.208	15.4	11 (12)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	22.9	6 (6)	95.45 %	mRNA binding	mRNA-nucleus export

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
PFK1/YGR240C	987	0.466	6.0	4 (4)	63.64 %	6-phosphofructokinase	glycolysis
PFK2/YMR205C	959	0.512	6.8	4 (4)	31.82 %	6-phosphofructokinase	glycolysis
PRB1/YEL060C	635	0.3	4.9	2 (2)	31.82 %	serine-type endopeptidase	sporulation*
RPL10/YLR075W	221	0.827	10.9	2 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL15A/YLR029C	204	0.783	20.6	0 (3)	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL15B/YMR121C	204	0.436	20.6	↑	36.36 %	struct. const. of ribosome*	protein biosynthesis
RPL18B/YNL301C	186	0.68	17.7	0 (3)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL18A/YOL120C	186	0.812	17.7	↑	31.82 %	struct. const. of ribosome	protein biosynthesis
RPL19B/YBL027W	189	0.708	13.2	0 (2)	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL19A/YBR084C-A	189	0.686	13.2	↑	50.00 %	struct. const. of ribosome	protein biosynthesis
RPL1B/YGL135W	217	0.832	12.0	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL1A/YPL220W	217	0.821	12.0	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL20A/YMR242C	180	0.665	17.2	0 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	17.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL21A/YBR191W	160	0.691	16.2	0 (3)	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL21B/YPL079W	160	0.733	16.2	↑	36.36 %	struct. const. of ribosome	protein biosynthesis
RPL25/YOL127W	142	0.748	18.3	2 (2)	54.55 %	struct. const. of ribosome*	protein biosynthesis*
RPL27B/YDR471W	136	0.517	18.4	0 (2)	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL27A/YHR010W	136	0.736	18.4	↑	27.27 %	struct. const. of ribosome	protein biosynthesis
RPL28/YGL103W	149	0.705	39.6	7 (7)	68.18 %	struct. const. of ribosome*	protein biosynthesis
RPL2A/YFR031C-A	254	0.773	4.3	0 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL2B/YIL018W	254	0.764	4.3	↑	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL3/YOR063W	387	0.83	17.1	5 (5)	40.91 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	31.9	1 (3)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	23.9	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL32/YBL092W	130	0.818	13.8	2 (2)	63.64 %	struct. const. of ribosome	protein biosynthesis
RPL4A/YBR031W	362	0.803	14.9	0 (3)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL4B/YDR012W	362	0.812	14.9	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	29.8	1 (8)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	29.8	1 (8)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPP0/YLR340W	312	0.794	12.2	3 (3)	45.45 %	struct. const. of ribosome	protein biosynthesis*
RPS15/YOL040C	142	0.769	16.9	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
RPS18A/YDR450W	146	0.775	31.5	0 (6)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	31.5	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS1A/YLR441C	255	0.696	9.4	1 (2)	40.91 %	struct. const. of ribosome	protein biosynthesis
RPS1B/YML063W	255	0.769	9.4	1 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPS20/YHL015W	121	0.827	22.3	2 (2)	31.82 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	19.2	0 (2)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	19.2	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS26B/YER131W	119	0.711	20.2	0 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS26A/YGL189C	119	0.781	20.2	↑	22.73 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	12.1	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*
SHM1/YBR263W	565	0.264	14.2	8 (8)	63.64 %	glycine hydroxymethyltransferase	one-carbon compound metabolism
SRO9/YCL037C	466	0.264	20.2	7 (7)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	14.8	1 (8)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	17.2	2 (9)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	6.9	0 (3)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	6.2	0 (3)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	16.0	0 (7)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	16.0	↑	59.09 %	chaperone*	protein biosynthesis
SVL3/YPL032C	825	0.164	4.1	2 (2)	27.27 %	mol. funct. unknown	endocytosis
TDH1/YJL052W	332	0.856	13.9	1 (3)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	17.2	0 (4)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	19.3	1 (5)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TEF2/YBR118W	458	0.876	7.9	0 (3)	90.91 %	translation elongation factor	translational elongation
TEF1/YPR080W	458	0.871	7.9	↑	90.91 %	translation elongation factor	translational elongation
UGP1/YKL035W	499	0.33	11.8	4 (4)	59.09 %	UTP–glucose–1–P_i uridylyltransf.	protein AA glycosylation*
URA2/YJL130C	2214	0.286	4.3	6 (6)	63.64 %	aspartate carbamoyltransferase	pyrimidine base biosynthesis
YAR009C	NF	NF	9.4	0 (7)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML045W	NF	NF	6.4	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YAR010C	NF	NF	13.4	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER137C-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-A	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YDR261C-C	NF	NF	13.4	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	4.7	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-A	NF	NF	8.6	0 (3)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER159C-A	NF	NF	8.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-A	NF	NF	8.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-C	NF	NF	8.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-A	NF	NF	8.6	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	6.2	0 (8)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	6.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	8.5	0 (10)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	8.5	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	8.5	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	9.7	0 (11)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	9.7	0 (12)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YEF3/YLR249W	1044	0.778	2.5	2 (2)	54.55 %	translation elongation factor	translational elongation
YER138C	NF	NF	9.7	0 (12)	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	8.1	0 (10)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-A	NF	NF	5.9	0 (2)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	7.9	0 (9)	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	4.0	0 (5)	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	6.1	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	4.8	0 (6)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	7.6	0 (9)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	7.6	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	6.7	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	7.6	0 (9)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	6.1	0 (8)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

26 TAP–MuDPIT analysis of immune precipitations with YNL116W–HPM as the bait protein

Table 62: Previously reported interaction partners of YNL116W according to MIPS (M), GRID (G) and YPD (Y) and their recovery by TAP–MuDPIT through a HPM–tag; column "Interaction" characterized the respective known interaction as "genetic" and/or "physical"; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;
listed interactors not retrieved by this experiment are: YCK1/YHR135C (M/G/Y, physical), YPL110C (G/Y, physical), CAR2/YLR438W (Y, physical), MDM30/YLR368W (Y, physical), GPD1/YDL022W (Y, physical), SEN1/YLR430W (Y, physical), GPD2/YOL059W (Y, physical), PDC6/YGR087C (Y, physical), RPT2/YDL007W (Y, physical), YAL027W (Y, physical), YHR033W (Y, physical), ERG1/YGR175C (Y, physical), SML1/YML058W (M/G/Y, physical), RPT4/YOR259C (Y, physical), SEC6/YIL068C (Y, physical), PIL1/YGR086C (Y, physical), MSI1/YBR195C (Y, physical), RAD1/YPL022W (G/Y, physical), RVB1/YDR190C (Y, physical), STI1/YOR027W (Y, physical), STH1/YIL126W (G/Y, physical), DUN1/YDL101C (Y, physical), CDC123/YLR215C (M/G/Y, physical), UTP4/YDR324C (Y, physical), YDR433W (M/G, physical), STE20/YHL007C (Y, physical), LSP1/YPL004C (Y, physical), THI4/YGR144W (M/G/Y, physical), FAR1/YJL157C (Y, physical), PHO84/YML123C (G/Y, physical);

Gene	Interaction	Database	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YNL116W	Bait	Bait	522	0.130	67.2	46 (49)	9.09 %	mol. funct. unknown	biological process unknown
UBI4/YLL039C	physical	Y	381	0.317	5.8	0 (2)	22.73 %	protein tagging*	response to stress*
RPL40A/YIL148W	N. A.		128	0.742	17.2	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis*
RPS31/YLR167W	N. A.		152	0.811	14.5	↑	31.82 %	struct. const. of ribosome*	protein biosynthesis*
RPL40B/YKR094C	N. A.		128	0.742	17.2	↑	18.18 %	struct. const. of ribosome*	protein biosynthesis*
SKP1/YDR328C	physical	Y	194	0.193	37.6	6 (6)	9.09 %	ubiquitin-protein ligase	ubiquitin–dep. prot. catabol.*
YHR115C	physical	G/Y	416	0.151	46.4	22 (25)	9.09 %	mol. funct. unknown	biological process unknown
YNL311C	physical	G/Y	763	0.141	27.8	19 (19)	9.09 %	protein binding	ubiquitin–dep. prot. catabol.

Table 63: Potential interactors recovered through TAP–MuDPIT on YNL116W–HPM; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
JIP5/YPR169W	514	0.166	5.6	2 (2)	9.09 %	mol. funct. unknown	biological process unknown

Table 64: Proteins which co–purify with YNL116W–HPM but are likely to be contaminants; gene products that were identified in more than 20% of 22 TAP–MudPIT analyses in this study were sorted to here; column "Length" is the ORF length in AAs according to SGD; column "CAI" represents the codon adaptiation index of the gene in question according to SGD; Column "Peptides" lists the number of filtered peptides assignable to the ORF; column "Frequency in Data Set" is the percentage of TAP–MudPIT analyses in this study in which the gene product was identified in ($n = 22$); columns "Function" and "Process" reflect functional annotation in SGD; data is filtered as given in section 1, page 7;

Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
CTS2/YDR371W	511	0.137	16.8	5 (5)	81.82 %	mol. funct. unknown	biological process unknown
ILV1/YER086W	576	0.312	9.9	3 (3)	45.45 %	threonine dehydratase	branched chain family AA biosynth.
MIS1/YBR084W	975	0.208	5.4	4 (4)	90.91 %	formate-tetrahydrofolate ligase*	nucleic acid metabolism*
NPL3/YDR432W	414	0.359	13.0	3 (3)	95.45 %	mRNA binding	mRNA-nucleus export
RPL20A/YMR242C	180	0.665	13.3	0 (2)	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL20B/YOR312C	174	0.697	13.8	↑	45.45 %	struct. const. of ribosome	protein biosynthesis
RPL30/YGL030W	105	0.865	27.6	2 (2)	22.73 %	struct. const. of ribosome	protein biosynthesis*
RPL31A/YDL075W	113	0.737	23.9	0 (2)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL31B/YLR406C	113	0.63	23.9	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPL9A/YGL147C	191	0.771	33.0	1 (4)	95.45 %	struct. const. of ribosome	protein biosynthesis
RPL9B/YNL067W	191	0.778	33.0	1 (4)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS15/YOL040C	142	0.769	21.1	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis
RPS18A/YDR450W	146	0.775	15.1	0 (2)	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS18B/YML026C	146	0.733	15.1	↑	68.18 %	struct. const. of ribosome	protein biosynthesis
RPS22A/YJL190C	130	0.812	12.3	0 (1)	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS22B/YLR367W	130	0.523	12.3	↑	90.91 %	struct. const. of ribosome	protein biosynthesis
RPS3/YNL178W	240	0.8	12.5	2 (2)	54.55 %	struct. const. of ribosome	protein biosynthesis*
SRO9/YCL037C	466	0.264	15.9	4 (4)	95.45 %	RNA binding	protein biosynthesis
SSA1/YAL005C	642	0.709	12.8	1 (6)	100.00 %	chaperone*	protein folding*
SSA2/YLL024C	639	0.802	15.2	2 (7)	100.00 %	heat shock protein	protein folding*
SSA3/YBL075C	649	0.177	5.1	0 (2)	81.82 %	heat shock protein	response to stress*
SSA4/YER103W	642	0.184	4.4	0 (2)	72.73 %	chaperone*	response to stress*
SSB1/YDL229W	613	0.82	5.1	0 (2)	59.09 %	chaperone*	protein biosynthesis
SSB2/YNL209W	613	0.772	5.1	↑	59.09 %	chaperone*	protein biosynthesis
TDH1/YJL052W	332	0.856	9.6	0 (2)	95.45 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH3/YGR192C	332	0.924	13.9	0 (3)	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
TDH2/YJR009C	332	0.905	13.9	↑	100.00 %	glyceraldeh. 3–P_i dehydrogenase	gluconeogenesis*
YAR009C	NF	NF	2.3	0 (2)	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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Gene	Length	CAI	Seq. Cov.	Peptides unique (all)	Frequency in Data Set	Function	Process
YML045W	NF	NF	1.5	↑	63.64 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YML039W	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR227W-B	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR157C-B	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YLR035C-A	NF	NF	2.3	↑	54.55 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR029W	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YJR027W	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YHR214C-B	NF	NF	1.5	↑	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR161C-D	NF	NF	1.5	↑	72.73 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR038C-B	NF	NF	1.5	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YGR027W-B	NF	NF	1.5	↑	77.27 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBL005W-B	NF	NF	2.2	0 (3)	68.18 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER160C	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YER138C	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR365W-B	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR316W-B	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR261C-D	NF	NF	2.4	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR210C-D	NF	NF	2.2	↑	81.82 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YDR098C-B	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)
YBR012W-B	NF	NF	2.2	↑	86.36 %	not in SGD (orf_geneontology.tab)	not in SGD (orf_geneontology.tab)

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